STIC-Biotech/ChemLib

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Whiteman, Brian Tuesday, August 12, 2003 9:43 AM STIC-Biotech/ChemLib

seq search

09/380,546 11/29/99 Wallach et al.

search seq id nos: 1-4 against us patent and us patent application databases

Thanks, Brian Whiteman, 11e12 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office Crystal Mall 1, 11A16 (703) 305-0775

Searcher:
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Location:
Date Picked Up: \(\frac{\gamma/13}{2} \)
Date Completed: 8/25
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Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Others

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Human apoptosis re Human Gl protein i

nove

cDNA encoding

Human MACH related Human MACH related Human MACH related Substance of FLIP-C encod Mouse FLIP-C encod Nucleotide sequenc Usurpin-gamma poly Human FLICE-like I Human FLIP-C encod

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G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
modulator; apoptosis; cell death; inflammation; tumour; HIV;
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator; cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer; immune disorder; rheumatoid arthritis; systemic lupus erythematosus; reproductive disorder; tumour; gastrointestinal disorder; cirrhosis; colitis; hepatitis; pancreatitis; ss.
                                                                                                                                                                                      Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
                                                                                                                                                 apoptosis associated protein HAPOP-1 encoding cDNA
                                        BP.
                                       AAZ47926 standard; cDNA; 2352
                                                                                                            10-MAR-2000 (first entry)
                                                                        AAZ47926
                                                                                                                                                   Human
RESULT 2
AA247926
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Homo sapiens

206 135 266 195 326 255 386 315 446 375 506 435

CTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGAGCACGGGAGGAGGTGTAGGA CTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGACCACGGGAGGAGGTGTAGGA GAGAAGCGCCGCGAACAGCGATCGCCCAGCACCAAGTCCGCTTCCAGGCTTTCGTTTCT

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The present sequence encodes a human apoptosis associated protein designated HAPOP-1. HAPOP proteins are apoptosis regulators which have antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic activity. A pharmaceutical composition mapped to activity. A pharmaceutical composition comprising HAPOP in conjunction with a carrier, a purified antagonist of HAPOP, vectors and agonists of HAPOP, are administered for diagnosing, treating or preventing disorders associated with increased or decreased apoptosis, e.g. call proliferative disorders such as rhematolal arthritis, systemic lupus erythematosus; reproductive disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as cirrhosis, colitis, hepatitis and pancreatitis. The polymuclocitides encoding HAPOP proteins may be useful to detect and quantitate expression of HAPOP genes which are correlated with diseases and are also useful to detect differences in the chromosomal location due to translocation, invession of the correlated with diseases and etc. the combination of the correlatic agents may act synergistically to effect the treatment or prevention of various disorders providing improved efficacy with lower dosages of each agent and thus reducing the potential for adverse side effects.
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                                                                                                                                                                                                                         Patterson C,
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                                                                                                                                                                                                                                                                                                                     New protein for diagnosing, treating o
with increased or decreased apoptosis
                                                                                                                                                                                                                         Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 71-72; 81pp; English.
                                                                                                  99WO-US10386
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                                                                                                                                                                               (INCY-) INCYTE PHARM INC
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Db 1586 TCAGACTCCGGGCTCCCCTGCATCACATCAGGAGGATGTTCATGGGAGATTCATG 1645 Qy 1516 CCCTTATCTAGGAGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGGTGTCAGAGGG 1575 Db 1646 CCCTTATCTAGGAGGCAAAGATGTTTTATATCAGAACTATGTGGTGTTAGAAGGGAAGCTAAAAGATTTTATTATTCAGAACTAGAAGGGAAAGTTTTAATCAGAACTAGTGGTGGTGGTGGTGGTGGTGGTGTAGTGGTGGTGGTG	QY 1576 CCAGCTGCAGAACAGCAGCCTCTTCGAGGTGGATGGGCCAGCGATGAAGAATGTGGAATT 1635	36 CAAGGCTCAGAAGCGAGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCTGGAGCCCT 16	96 26	9 9	Qy . 1816 ACTCAATGCTACATGTATGGAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGT 1875	1876	QY 1936 GCTGGGCGTAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGAGGCCAGAT 1995	Qy 1996 CACTTCAGGTCAGGAGTTCGAGGACCTGGCCAACATGGTAAACGCTGTCCCTAGTAA 2055 .	2056 A 1 2186 A	QY 2116 TGAGGTGGGAGGATCTTTGAACCCAGGAGTTCAGGGTCATAGCATGCTGTGATTGTGC 2175	Qy 2176 TACGAATAGCCACTGCATACCAGGCAATATAGCAAGATCCCA 2222 	RESULT 3 AAV31375 ID AAV31375 standard; cDNA; 2188 BP.	XX AC AAV31375; XX DT 07-SEP-1998 (first entry)	<pre>Human FIN-1 encoding cDNA. Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector dom</pre>	<pre>KW apoptosis related protein; caspase; viral infection; cancer; tumour; KW diagnosis; ischaemic injury; neuro-degenerative disorder; ds. XX OS Homo sapiens.</pre>	Key . Location/Qualific CDS 4221864 /*tag= a	/produ EP841399-A2.
	566 AGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGCTGCTGAAGT 625 496 CATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGGAGATGCTGCTGCTCTTTTGTG 555 1111111111111111111111111111111111	CCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTTCTGGATATTTTACG 61	67	CTCAG 73 11111 CTCAG 86	TTGGA 79 TTGGA 92	AAGAT 85 AAGAT 98	91	CCCAGATCACTGGATTTATTAGAAAATGCCTAAAGAACATCCACAGAATAGACTGAA 975 	GACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGGAGGAGGAGTACAGGAATGT 103	TCTCCAAGCAGCAATCCAAAAGGTCTCAAGGATCCTTCAAATAACTTCAGGCTCCATAA 109 	Grgaa 1	1156 GAAATCCATTCAGGAATCAGAAGCTTTTTGCCTCAGAGCATACCTGAAGAGAGATACAA 1215 	1216 GATGAAGAGCACAGGAATCTGCCTGATAATCGATTGCATTGGCAATGAGACAGA 1275 	1276 GCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATTCTTGCATCTCAG 1335 	1336 TATGCATGGTATATCCCAGATTCTTGGCCAATTTGCCTGTATGCCCGAGCACCGAGACTA 1395 	1396 CGACAGCTTTGTGTGTGTCCTGGTGAGCCGAGGGCTCCCAGAGTGTGTATGGTGTGGA 1455 	1456 TCAGACTCACTCAGGCTCCCCCTGCATCACAGGAGGATGTTCATGGGAGATTCATG 1515

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                                                                                                                                                                                                                                                                                       The present sequence encodes human FIN-1 (FLICE inhibitor-1), which is a caspase. FLICE (ICE-IAP7) is a protease of the interleukin-converting enzyme family, a protein involved in the regulation of cell death. A host cell, comprising a vector containing FIN-1 encoding DNA, can be used to produce FIN-1. The vector containing the DNA can be used for producing a cell which expresses a polypeptide by transforming or transfecting the cell with it so that the cell expresses the polypeptide or transfecting the cell with it so that the cell expresses the polypeptide or transfecting the cell with it so that the cell expresses the polypeptide or to antagonist can be used in the vector. The polypeptide or its invivo administration. Conditions which may be treated include viral infection, tumours (especially solid tumours), ischaemic injury (e.g. stroke or myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or Parkinson's disease, osteoarthritis, polycystic kidney disease, chronic degenerative liver disease, acquired immunodeficiency syndrome (AIDS) and aplastic anaemia the
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tumour, ischaemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides may also be used for chromosome identification
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                                                                                                                                                                                                 New nucleic acid encoding human apoptosis-related diagnosis and treatment of e.g. viral infections, injury and neuro-degenerative disorders
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                                                                                                                                                                                                                                                            Claim 4; Page 22-25; 48pp; English.
                                                                                                BEECHAM CORP
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99.8%;
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                                                                  96US-0748086
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P-PSDB; AAW58578.
                                                                                                                             Emery JG, Kikly K;
                                                                                                (SMIK ) SMITHKLINE
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                                      10-NOV-1997;
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                                                                                          /product= "FLICE-like inhibitory protein long form" /note= "FLIP-L; apoptosis inhibitor"
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                                                                                                                                                                                                                                              Claim 14; Page 68-69; 105pp; English.
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99.78;
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Matches 2138; Conservative
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P-PSDB; AAY57454.
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negative regulator of caspase 8, File-C, where (1) specifically hardiases with and inhibits expression of the protein, or specifically hyridiases with at least an 8-nucleobase portion of an active site on (11). (1) has antinflammatory and anti-tumour activities. (1) is an inhibitor of File-c expression, a modulator of apoptosis and can be used in attisense gene therapy. (1) is useful for inhibiting the expression of File-c in cells or tissues, and for treating an animal having a disease or condition associated with File-c. (1) is also useful for modulating apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or caspase 7 is activated, and the File-c. (1) is also useful for diagnostics, therapputics, prophylaxis, as research reagents and kits, for distinguishing functions of various members of a biological pathway, and in antisense gene therapy. (1) is also useful complylactically, e.g., to prevent or delay infection, inflammation or tumour formation. The present sequence encodes human File-c as given in an example from the present invention. targeted to a nucleic acid molecule (II) encoding a natural dominant \$

Sequence 2143 BP; 590 A; 482 C; 576 G; 495 T; 0 other;

218 240 300 458 578 638 539 758 629 ATAGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCTCATTAA 719 TTTTCCTCATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGG 878 99 TAGGGGTGGGGACTCGGCCTCACACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGAC 158 AGCTGAGACAACAAGGACCACGGGAGGAGGTGTAGGAGAAAGCGCCGCGAACAGCGATC 120 TCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAGTCCGGCCGCGACA 338 GGACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAA 398 GGGACTTGGCTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGA 698 9 AGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACT TICCACCIAAIGICAGGGACCIICIGGAIAITITACGGGAAAGAGGIAAGCIGICIGICG <u> AGCTGAGACAACAAGGACCACGGGAGGAGGTGTAGGAGAGAAAGCGCCGCGAACAGCGATC</u> GCCCAGCACCAAGTCCGCTTCCAGGCTTTCGGTTTTCTTTGCCTCCATCTTGGGTGCGCCT GTTGACTGCCTGCTGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTG TTGATACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGG Gaps 1; Score 2124; DB 24; Length 2143; Pred. No. 0; Indels 5, 0; Mismatches Query Match
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Matches 2138; Conservative 159 61 420 639 540 009 279 339 399 301 459 519 579 480 669 759 819 219 셤 셤 g ò 셤 à g δ 셤 ò a ò a g 셤 å 엄 ò à ð δ õ

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QY	1419	AGCCGAGGAGCTCCCAGAGTGTGTATGGTGGATCAGACTCACTC	478
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οy	1479	GCATCACATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGAAGCCAA 1	538
qq	1380	GGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAA 1	439
δλ	1539	AGATGTTTTTATTCAGAACTATGTGGTGTCAGAGGGCCAGCTGGAGAACAGCGCCCCT 15	598
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οy	1599	GAGGTGGATGGGCCAGCGATGAAAGAATGTGGAATTCAAGGCTCAGAAGCGGGGGTGT 1	.658
đ	1500	AGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGTGT 1	559
δλ	1659	GCACAGTTCACCGAGAAGCTGACTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGC 17	718
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δŽ	1719	TGGAGCAGTCTCACAGCTCACCGTCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGAC 17	778
Q	1620	GGAGCAGTCTCACAGCTCACCATCCCTGTACCTGCAGTGCCTCTCCCCAGAAACTGAGAC 1	629
Qy	1779	SAAAGAAAACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTATGATT 1	1838
ପ୍ର	1680	AAAGAAAACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTATGATT 1	1739
δŏ	1839	AACAGCAGAGTTTCTGCCAAGGAGAATATTATGTCTGGCTGCAGCACACTCTGAGAA 1	8681
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                       1980 GGGTGTGGGTACCTGTATTCCCAGTTACTTGGGAGGTGAGGTGGGAGGATCTTTTGAAC
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compain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The proteins can inhibit both TYRR-1 and CD-95 induced apoptosis. These are the first examples of a naturally occurring catalytically inactive caspase that can act as a dominant negative inhibitor of apoptosis. The polypeptides and agonists can be used for treating e.g. Alzheimer's disease, Parkinson's alsease, rheumatoid arthritis, septic shock, sepsis, stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury, cell death associated with cardiovascular disease, polycystic kidney disease, apoptosis of endothelial cells in cardiovascular disease, cell death associated with polypeptides can be used for treating cancers (e.g. follicular lymphomas, carcinomas with p53 mutations.) cell for follicular lymphomas, carcinomas with p53 mutations. Inver, lung, pancreas, and cancers of the breast, ovary, prostate, bone, liver, lung, pancreas, and spiden), autoimmune disorders ceg. systemic lupus erythematosus, immune-related glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis), and viral infections (e.g. herpes viruses, pox viruses and adenoviruses), graft versus host disease, acute disease, acute graft rejection, and chronic graft rejection. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                            I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's diseas CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis; CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease; multiple sclerosis; head injury; cancer; autoimmune disorder; therapy; viral infection; graft versus host disease; graft rejection; ss.
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treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis,
cancers, autoimmune disorders, viral infection or graft rejection
Rosen CA;
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/product= I-FLICE-1
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                                                                                         AAV44806 standard; DNA; 2034
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97US-0034205
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                                                                                                                                                                                               I-FLICE-1 coding sequence.
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DB 19; Length 2034;

560 A; 456 C; 540 G; 478 T; 0 other;

Sequence 2034 BP;

Score 2006.8;

89.58;

Query Match

CAACAAGGACCACGGGAGGAGGTGTAGGAGAGAAGCGCCGCGAACAGCGATCGCCCAGCA

167

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This sequence encodes the human CLARP protein. The invention relates to the human RICK (RIP-like interacting CLARP kinase) protein. The RICK the human RICK (RIP-like interacting CLARP kinase) protein acts as a positive requiator of apoptosis, potentiating apoptosis induced by caspase-8 and capase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors of row provides methods and compositions of the various compositions and activators, and methods and compositions of the various compositions of the interactions of the various compositions of the interactions of the various compositions of the interactions of the various compositions of and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CIARP can be used in drug screening assays to identify inhibitors of the enzymatic of noting by the complexes containing RICK and containing to growth and dysregulation of ARC-like inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitors compositions of containing useful for gene therapy treatment of disease with increased cell disease. Antirick antibodies can be used discreters, aphastic anaemia, ischaemic injury, and toxin-induced liver of alsomates. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as apoptosis is neceded. RICK interaction with intracellular factors of RICK binding to intracellular apoptosis factors are potential drug candidates.
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                                                                    RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-8; NERP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
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99.0%; Pred. No. 0;
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Matches 2003; Conservative
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Chaudhary PM;
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      ATAATCGATTGCATTGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGC
                    TATGAAGTCCAGAAATTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTTGGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AlDS; aplastic anaemla; myocardial infarction; therapy; ss.
                                                                                                                       GCCAACATGGTAAACGCTGTCCCTAGTAAAAATGCAAAAATTA 2069
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The present sequence represents DNA coding for MACH-related inducer of toxicity (MRIT) isoform MRIT alpha 1 (see AAY05787), a CED-4 chamily polypeptides, and which has pro-apoptotic activity. An EST sequence having homology to the p20 domain of human ICE-like protease MACHL/FLICE was isolated from an EST database. Several coverlapping EST clones were sequenced to deduce the sequence of the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see AAX5509) and beta 1 (see AAX5510). The MRIT alpha 1 includes an N-terminal death effector domain and a C-terminal caspase homology domain, but is not a cysteine protease. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell anthibitors of programmed cell death. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, angiogenesis and atherosclerosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzieniems's disease, parkinson's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic
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Pred. No. 0;
0; Mismatches 4; Indels 1: 6
                                                                                                                                                                                                                                                                                                 Identifying regulators of MACH.-related inducer of toxicity
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Best Local Similarity 99.7%;
Matches 1992; Conservative
97US-0946226
                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                 WPI; 1999-277275/23.
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CTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACA
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                                                                                                                                                                       This cDNA clone includes a coding region for a novel human protein (see AAW6915), designated Casper (for caspase-eight-related protein), that is involved in regulation of apoptosis. The clone was involved in regulation of apoptosis. The clone was cloated from a human expressed sequence tag database in a search for potential FADD-related genes. The isolated protein, or cells that express the protein, can be used to screen for agents, cells that express the protein, can be used to screen for agents, cells and thus its function. Nucleic acid sequences encoding Casper to a target, and thus its function. Nucleic acid sequences and primers for diagnostic detection of Casper genes and primers for diagnostic detection of casper genes and to their transcripts, for isolation of related sequences and for the modulate expression of active Casper protein (using antisense or sense sequences). They are also used for recombinant production of Casper and to generate transgenic animals for testing candidate
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isolate similar
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or
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
87.0%; Score 1952.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1965; Conservative 0; Mismatches
                                                                                                 New Casper protein involved in regulation
to identify specific modulators, identify
sequences and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                            drugs for Casper-associated diseases
                                                                                                                                                    Claim 7; Page 21; 29pp; English
                                                           WPI; 1998-437440/37
P-PSDB; AAW69715.
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present sequence represents

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides recombinant nucleic acid molecules encoding usurplin-alpha (lacking the first death effector domain (DED) or its prodomain), usurplin-beta or usurphin-game. Usurplin polypeptides are useful for in vitro and in vivo identification of usurpin-procaspase-8 interaction inhibitor. Usurpin is useful as modulator of the sensitivity of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis is useful for treating diseases like autoimmune diabetes, cancer and parkinson's disease. Activators and inhibitors of usurpin-procaspase-8 interaction are also useful for treating various diseases mediated by apoptosis. Usurpin provides an attractive model for modulating caspase activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be regulated at several levels in the presence of usurpin, conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta; usurpin-qamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA molecules and polypeptides for treating apoptosis e.g. autoimmune diabetes, cancer and Parkinson's
                                      AACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTATGATTGGAACAGCA
                                                                                                                                               GAGITICIGCCAAGGAGAAATAITAIGICIGGCIGCAGCACCICIGAGAAAGAAACITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; im
caspase; cytostatic; antiParkinsonian; antidiabetic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Usurpin-alpha polypeptide encoding cDNA.
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                                                                                                                  CAGGIIGAAGAAGCACIIGAIACAGAIGAGAAGGAGAIGCIGCICIIIIIGIGCCGGGAI
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                                                                                         287 CAGCAGGTCTGAGCTTGTCCGGCGAGGGTGGGAGTTGGTCCCGGCGGAGATCCAGTGGGA
                                                                                                         AGCCCTCAGAAATGAAGTTGACTGCCTGCTGGCTTTCCTGTTGACTGGCCCGGAGCTGTA
                                                         Gaps
                                        2084;
                                                        ;
                                        Length
                                                         Indels
                        Sequence 2084 BP; 553 A; 475 C; 565 G; 491.T; 0 other;
                                         DB 21;
                                                         49;
resistance to Fas-ligand cell death. The pre CDNA encoding the usurpin-alpha polypeptide
                                                 Pred. No. 0;
0; Mismatches
                                        Score 1708.6;
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                                       Query Match 76.2%;
Best Local Similarity 97.2%;
Matches 1749; Conservative
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This cDNA sequence codes for human FLAME-1 (see AAW90107), or FADD-11ke apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic protein that interacts specifically with FADD, Nch4, anti-apoptotic protein that interacts specifically with FADD, Nch4, anti-apoptotic protein that interacts specifically with FADD, Nch4, can abrogate Fas/TNR-induced apoptosis upon expression in Fas/TNR-sensitive MCF-7 cells. The FLAME-1 gene was mapped to chromosome 2q3-34. The full-length FLAME-1 cDNA was isolated from a Jurkat cDNA interaction of taself been generated from the Jurkat library using primers (see AAV94139-42) based on an isolated EST clone. Host cells, recombinant vectors, and methods of using FLAME-1 to identify substrates, activators or inhibitors of FLAME-1 are provided. FLAME-1, activators or inhibitors of FLAME-1 are provided FLAME-1, cells, recombinant et frame and methods and agonists can be used to inhibit apoptosis, coff the polypeptides can be used for gene therapy, e.g. antisense cold molecules can be used in vivo for antineoplastic purposes.
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                                                                                                                                                                                                                                                                                       New isolated FADD-like anti-apoptotic molecules - used to capoptotic and anti-apoptotic agents for treating, e.g. HIV infection, Alzheimer's disease or neoplastic conditions
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The invention relates to FADD-like apoptotic/anti-apoptotic proteins (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME sequences are useful for inhibiting apoptosis and for gene therapy of diseases characterised by apoptosis including HIV infection and Alzhelmer's disease. FLAME inhibitors are useful as apoptotic agents and activators are useful as anti-apoptotic agents. FLAME-1 is useful as a bubstrate for caspase in assays to identify caspase inhibitors. The present sequence is human FLAME-1 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport group
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                                                                      Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte; tumour specific antigen; immune response; therapy; prophylaxis; diagnosis; HIV; human immunodeficiency syndrome; AlDS; acquired immune deficiency syndrome; human; ds.
                                                                                                                                                                                                                                                                                                       FLICE like inhibitor protein and detectable peptide tag
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                                     FLIP with detectable amino acid coding sequence.
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(ALGE/) ALGECIRAS-SCHMINICH A.
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Matches 1441; Conservative
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Best Local Similarity 99.8%;
Matches 1302; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive;
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                        TTCTTCTGGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCG
                                                                     Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta; usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppres; caspase; cytostatic; antiParkinsonian; antidiabetic; ss.
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1020	1561	1080	1621	1140	1681	1200	1741	1260			
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SUMMARIES

criptic	AR6556 Sequence 1 BD105908 CASH(Casp Y14039 Homo saplen A84918 Sequence 9 BD107658 FLIP gene U97074 Homo saplen BD056976 I-FLICE, BC001602 Homo saplen AR19434 Sequence AR005774 Homo saplen AR196902 Sequence AR005774 Homo saplen AR196902 Sequence AR005774 Homo saplen AR19605774 Homo saplen AR1960578 Homo saplen BD003439 FADD-11ke AR01545 Homo saplen BR005751 Homo saplen AR01545 Homo saplen BR005751 Homo saplen AR01545 Homo saplen AR01545 Homo saplen AR01545 Homo saplen AR01545 Homo saplen AR01659 FLIP gene BR005697 I-FLICE, AR01145 Sequence 12 BD107659 FLIP gene BR005697 I-FLICE, AR01145 Sequence 12 BD107659 FLIP gene BR005697 I-FLICE, AR01145 Sequence AX51144 Sequence AX51145 Sequence AX51146 Sequence AX51146 Sequence AX51147 Homo saplen BR005697 FLIP gene BR005697 FLIP gene AR01545 Homo saplen AR01545 FLIP gene	NA linear PAT 21-JAN-2000 EFFECTOR DOMAIN, MODULATORS OF
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DEFINITION ACCESSION VERSION

RESULT 3 HSY14039 LOCUS

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Brodianskii,V.M. and Wallach,D.
CASH, a novel caspase homologue with death effector domain:
J. Biol. Chem. 272 (32), 19641-19644 (1997)
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JP 2002501371-A/2
15-JAN-2002
31-MAR-1998 JP 1998541154
01-APR-1997 DE 197 13 393.2
JURG TSCHOPP, MARGOT THOME, KIMBERLY BURNS, MARTIN IRMLER, MICHAEL
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/organism='Homo sapiens, long version
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C12N15/12,C07K14/47,C12N5/10,G01N33/68
Strandedness: Single;
Topology: Linear;
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Tschopp,J., Thome,M., Burns,K., Irmler, Schneider,P., Bodmer,J.L., Steiner,V., French,L.E.
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Pred. No. 0;
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/organism="unidentified"
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FLIP gene and FLIP protein BD107658 1 GI:23202476 JP 2002501371-A/2. Unidentified unidentified unclassified.
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KEYWORDS
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REGGLISVGDLAELLYRNRPREGKIRRILERSFLDLVVARDGLDLERCLKNIH
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AQQEPWKSIQESAFLPGSTRNVLQAALQKSLRDFFSLGY
ROQKFLHLSMHGISOJLGGPRCMPBEHBDYDSFVCVLVSRGGSOSVYGYDOTHSGLDLH
HTRNFMGDSCPYLAGKPREFFIQNTVVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGL
CTVHREADFFWSLCTADMSLLEGGSHSSPSLYLQCLSQKLRQERKRPLLDLHIELNGYM
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            Schneider, P., Hofmann,
       Irmler, M., Thome, M., Hahne, M., Schneider, P., Hofmann Steiner, V., Rimoldi, D. and Tschopp, J.
Direct Submission
Submitted (11-APR-1997) Biochemistry, University of des Boveresses 155, Epalinges, VD 1066, Switzerland
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383. .1825
/note="FLIP-L; apoptosis inhibitor"
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2138; Conservative 0; Mismatches
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1 (bases 1 to 2143)

1 (bases 1 to 2143)

1 (ranler, M., Thome, M., Hahne, M., Schneider, P., Hofmann, K., Steiner, V., Bodmer, J.L., Schroeter, M., Burns, K., Mattmann, C., Rimoldi, D., French, L.E. and Tschopp, J.

Inhibition of death receptor signals by cellular FLIP 97360133

9217161
                                                                                                                                                                                                                                       1920 CCAGCCTGGCCAACATGGTAAACGCTGTCCCTAGTAAAAATACAAAATTAGCTGGGTGT
                                                                                                                                                                                              GGAACAGCAGAGTTTCTGCCAAGGAGAATATTATGTCTGGCTGCAGCACACTCTGAGAA
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                 TGGAGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGT
   TGCATCACATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAA
                                                           AGATGTTTTTTATTCAGAACTATGTGGTGTCAGAGGGCCAGCTGGAGAACAGCAGCCTCT
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Homo sapiens FLICE-like
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VERSION KEYWORDS

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Oy 1234 AGGAATCTGCCTGATAA)	Qy 1294 CACTTCCCTGGGCTATG. 1 1 1 1 1 1 1 1 1	Qy 1354 GATTCTTGGCCAATTG 	Oy 1414 CCTGGTGAGCCGAGGAG	1474 C	1260	Qy 1534 GCCAAAGATGTTTTTA 	Qy 1594 CCTCTTGGAGGTGGATG	1380	DD 140 GCTGTGCACAGTTCACC	Qy 1714 CCTGCTGGAGCAGTCTC.	1500	Db 1560 GAGACAAGAAAAA		1620	Db 1680 GAGAAACTTATCC	Oy 1954 CACCTGTAATCCCAGCA	1740	Oy 2014 CGAGACCAGCCTGGCCA 11111111111111111111111 Db 1800 CGAGACCAGCCAGCCAG	2074	1860	OY 2134 TGAACCCAGGAGT	20	Qy 2194 ACCAACTGGGCAATAT	RESULT 8	LOCUS BC001602 DEFINITION Homo sapiens, Simil
Query Match 89.5%; Score 2006.8; DB 6; Length 2034; Best Local Similarity 99.6%; Pred. No. 0; Matches 2022: Conservative 0: Mismatches 7: Indels 1: Gans 1:	GCCCAGCACCACCACTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTG 27	CGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAGTCCGGCCG 33	61 CGCCTTCCCGGCGTCTAGGGGAGGCGAAGGCTGAGGTGGCAGGGGGGAGAGTCCGGCCG 120 334 CGACAGGACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAA	CGACAGGACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAA	394 ATGAAGTTGACTGCCTGCTTTCCTGTTGACTGGCCCGGGGGTGTACTGCAAGACCC 453	TTGTGAGCTTCCCTAGTCTAAGATGTAGGATGTCTGCTGAAGTCATCCATC	240 TIGIGAGCTICCCIAGICIAAGAGIAGGAIGICIGCIGCAAGICCAICCA		TGTGGTTCCACCTAATGTCAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAGCTGTC	4T	TGTCGGGGGACTTGGCTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGGTCAAACGTAT 47	694 CTTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTC 753 	GGACTATAGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAAATCTGATGTGTCTC 81		ATTANTITICCICATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGTTT 87	buu artaartitecetcargaagaartacarggacccaaggcaagaraagaagaagaagargaagagariti 055 874 ctrggaactrgggaggagagagagaaaactaaaattrggtrgccccaagarcaagagagtr 933	CTTGGACCTTGTGGTTGAGTTGGAGAACTAAATCTGGTTGCCCCAGATCAACTGGATTT 71	934 ATTAGAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTA 993	720 ATTAGAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTA 779	CAAGCAGTCTGTTCAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCA 10	CAAGCAGTCTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCA 839	1054 AAAGAGTCTCAAGGATCCTTCAAATAACTTCAGGCTCATAATGGGAGAAGTAAAGAACA 1113 AIAIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1114 AAGACTTAAGGAACAGCTTGGCGCTCAACAAGAACCAGTGAAGAAATCCATTCAGGAATC 1173	AGAAGCTTTTTGCCTCAGGCATACCTGAAGAGAGAGATACAAGATGAAGAGCATTTTTTTT	960 AGAAGCTTTTTGCCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCT 1019
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/VDWNSRVSAKEKYYVWLQHTLRKKLILSYT"
                                                                                                                                                                                                                                       Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
infoebcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readam Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticla Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                           Euteleostomi;
                                                                                                                                                    Direct Submission
Submitted (03-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCACCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCC
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/product="Similar to CASP8 and FADD-like apoptosis
                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"

/clone="MGC:2044 IMAGE:3542993"

/clone="Lib="NIH MGC_8"

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MGC:2044 IMAGE:3542993, mRNA, complete cds
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Pred. No. 0;
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99.7%;
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Strausberg, R.
                                                            sapiens (human)
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Nunez,G., Inohara,N. and
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Homo sapiens caspase-like apoptosis regulatory protein (clarp) mRNA, alternatively spliced, complete cds.
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AQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGY
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CTVHRREADFFWSLCFAMSLLEQSHSSPSLYLQCLSGYKLRQERKRPLLDLHIELNGYM
YDWNSRVSRKEKYYVWLQHTLRKKLILSYT*
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Inohara,N., Kosekl,T., Hu,Y., Chen,S. and Nunez,G.
CLARP, a 'death effector domain-containing protein interacts with
caspase-8 and regulates apoptosis.
Proc. Natl. Acad. Sci. U.S.A. 94 (20), 10717-10722 (1997)
                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 2040)
Inohara,N., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
Direct Submission
Submitsed (28-MAY-1997) Department of Pathology, University of
Michigan Medical School, 1150 W. Medical Center Dr., C558 MSRBII,
Ann Arbor, MI 48109, USA
Location/Qualifiers
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/gene-"clarp"
/note-"clarp; alternatively spliced"
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/organism="Homo sapiens"
/organism="Emono sapiens"
/ol_xref="taxon:9606"
/chromosome="2"
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Direct Submission
Submitted (23-JUN-1997) Biology, Tul
South San Francisco, CA 94080, USA
Location/Qualifiers
1. 2039
/organism="Homo sapiens"
//db_xref="taxon:9606"
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1 (bases 1 to 2056)
Srinivasula, S.M., Ahmad, M., Ottilie, S., Bullrich, F., Banks, S., Armstrong, R.C. and Alnemri, E.S.
Frandes-Alnemri, T., Croce, C.M., Litwack, G., Tomaselli, K.J., Armstrong, R.C. and Alnemri, E.S.
FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates J. BAJTNFR1-induced apoptosis
J. Blol. Chem. 272 (30), 18542-18545 (1997)
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/function="anti-apoptotic molecule"
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Submitted (18-JUN-1997) Microbiology and Immunology, Thomas, Jefferson University, Kimmel Cancer Institute, 233 S. Tenth, Street, Philadelphia, PA 19107, USA
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Alnemri,E.S.
FADD-like anti-apoptotic molecules, methods of using the same, and compositions for and methods of making the same Patent: US 6207801-A 1 27-MAR-2001;
Location/Qualifiers
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qq	1018	103
οy	1209	ATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATG 1260
QQ	1035	ACAAGATGAAGAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATG 109
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ΟY	1329	GCCCGAGCACC 138
qq	1155	CICAGIAIGCAIGGIAIAICCCAGAIICIIGGCCAAIITGCCIGIAIGCCCGAGCAC
Qy	1389	GAGACTACGACAGCTTTGTGTGTGTGTCCTGGTGAGCCGAGGAGGCTCCCAGAGTGTGTATG 1448
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Qy	1449	i.
οp	1275	TGTGGATCAGACTCACTCAGGGCTCCCCTGCATCACATCAGGAGGATGTTCATG
ΟY	20	TGTGGTGT 156
qq	1335	ICATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTTT
Qy	1569	~
QQ	1395	CAGAGGGCCAGCTGGAGGACAGCACCTCTTGGAGGTGGATGGGCCAGCGATGAAGAATG 145
Qy	1629	TGGAATTCAAGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCT 168
qq	1455	IGGAATICAAGGCICAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCT 151
οy	1689	GGAGCCTGTGTACTGCGGACATGTCCCTGCTGCAGCAGTCTCACAGGTCACCGTCCGT
qq	1515	GGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACGCTCC
Qy	1749	
qa	1575	ACCIGCAGIGCCICTCCCAGAAACIGAGAAAGAAAAGAAA
Qy	1809	ACATIGAACICAAIGGCIACAIGTAIGAITGGAACAGCAGAGTIICIGCCAAGGAGAAI 18
QQ	1635	ACATTGAACTCAATGGCTACATGTATGGAACAGCAGAGTTTCTGCCAAC
QY	1869	ATTATGTCTGCTGCACACACTCTGAGAAGAAGAACTTATCCTCTTCTACACATAA 1924
Op	1695	ATTATGTTTGGCTGCAGCACTCTGAGAAAGAAACTTATCCTCT

Search completed: August 22, 2003, 11:36:38 Job time : 8385.31 secs

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Run

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1071)

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AL526318
SAL526318.2 GI:31064178
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Copyright (c) 1993 - 2003
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gb_est4:*
gb_est5:*
em_estfun:*
em_estfun:*
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em_gss_pln:*
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2243
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em_esthum:*
em_estin:*
em_estov:*
em_estov:*
em_estpl:*
em_estro:*
em_htc:*
gb_est1:*
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gb_htc:*
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41.6
40.3
39.2
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Sequence:
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933.8
904.4
879
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Maximum DB :
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No.
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BU500866 AGENCOURT AI683026 tw48e05.x BG250588 602362767 CA848651 1937e10.y BE304652 601106166

A1132915 HA1497 HU CB158243 K-EST0217 AW856737 RC3-CT029 A1921624 wo27h03.x

EST 23-MAY-2003

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BM477369.1 GI:18526411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.6%;
llarity 96.5%;
Conservative
                                                                                                                                                                                                                                                   Homo sapiens (human)
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Best Local S:
Matches 979
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881
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                              ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                       RESULT 2
BM477369
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                                       /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSOBCOLGYOO6"
/clone="Lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone="lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lib="tand cDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCXVSPORT 6 vector. Library was normalized.
a 228 c 295 g 244 t 8 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGCCTCATTAATT
                                                                                                                                                                                                               GGGGTGGGGACTCGGCCTCACACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACAG
                                                                                                                                                                                                                                                                CCGGCGTCTAGGGGAAGCCTGAGGTGGCAGGGCAGGAGTCCGGCCGCGACAGG
                                                                                                                                                                                                                                                                                                                                              ACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGT
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InvitroGen Corporation 1600 ID : CSODC016BH03QP1.
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                                                                                                                                                                       1071;
                                                                                                                                                                          Length
                                                                                                                                                                                            Indels
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                                                                                                                                                                       Score 982.2; DB 9
Pred. No. 4.6e-23;
6; Mismatches 4,
  http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualifiers
                                                                                                                                                                          43.8%;
98.8%;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                  Best_Local Similarity
Matches 1003; Conserv
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/lab_host="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/clone_lib="NHH_MGC_85"
/note="organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 GATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGAT
                                                                      ğ
                                   CITGIGGITGAGITGGAGAAACTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAA
CTIGIGGTIGAGITGGAGAAACTAAATTIGGTIGCCCCAGAICAACTGGATTIATTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAAGGATCCTTCAAATAACTTCAGGCTCCATAATGGGAGAAGTAAAGAACAAA 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12272 row: e column: 04
High quality sequence stop: 758.
                                                                                                                                                                                                                                          Length 1020;
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Pred. No. 1.5e-21;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata,
Mammalia, Eutheria, Primates, Catarrhin
                                                                                                                                                                                                                                                                                                                                                1020 bp
AGENCOURT 6484919 NIH_MGC_85 Homo
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5554155"
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REFERENCE 1 (bases 1 to 1201) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Contact Converted to the contact of t	http://fullength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO60ACO6NP1. Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers / Organism="Homo sapiens" / MD_LYpe="MRNA" / MD_LYpe="MRNA" / AD_Arref="taxon:960" / Clone="CSODIO6OYEII" / Lissue_type="PLACENTA COT 25-NORMALIZED" / Clone="List" Fine most applens PlaceNTA COT 25-NORMALIZED" / Clone="List" Fine most applens PlaceNTA Associated with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized." ORIGIN ORIGIN	Ouery Match 40.3%; Score 904.4; DB 9; Length 1201; Best Local Similarity 96.6%; Pred. No. 1.1e-20; Matches 952; Conservative 11; Mismatches 19; Indels 4; Gaps 4; Qy 1056 AGAGTCTCAAGGATCCTTCAAATAACTTCAGGCTCCATAATGGGAGAAGTAAAGAACAA 1115		1416 Transcream 1416
601 TCTGGATATTTACGGGAAAGAGGTAAGCTGTCTGTGGGGGACTTGGCTGACTGTTA 111 <t< td=""><td> GGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTCTTGGACCTTGTGGTTGAGTTGGAGAA </td><td>1081 CTTCAGGCTCCATAATGGGAGAAGTAAAGACTAAGGAACAGCTTGGGGCTCA 1140 </td><td> </td><td>AL551989, aL551989 1201 bp mRNA linear EST 31-MAY-2003 LOCUS AL551989 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONG CSODIOGOYEll 3-PRIME, mRNA sequence. AL551989 GI:31273805 AL551989 AL551989 GI:31273805 AL551989 GI:31273805 AL551989 GI:31273805 AL551989 BST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (capacity Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</td></t<>	GGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTCTTGGACCTTGTGGTTGAGTTGGAGAA	1081 CTTCAGGCTCCATAATGGGAGAAGTAAAGACTAAGGAACAGCTTGGGGCTCA 1140		AL551989, aL551989 1201 bp mRNA linear EST 31-MAY-2003 LOCUS AL551989 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONG CSODIOGOYEll 3-PRIME, mRNA sequence. AL551989 GI:31273805 AL551989 AL551989 GI:31273805 AL551989 GI:31273805 AL551989 GI:31273805 AL551989 BST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (capacity Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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659 TACAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTG 718
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                                                                                                                                                                                          Gaps
     this
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Superscript II RT (Life Technologies). Note:
NIH_MGC Library."
196 c 261 g 220 t 1 others
                                                                                                                                 Length 929
                                                                                                                                                                                          Indels
                                                                                                                                                                                               11;
                                                                                                                                    Score 879; DB 13;
Pred. No. 7.7e-20;
0; Mismatches 11;
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Local Similarity 98.5%;
hes 918; Conservative
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 927)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMS18 row: m column: 16
High quality sequence start: 4
High quality sequence stop: 632.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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Homo sapiens cDNA clone IMAGE:5550264
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apercourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12262 row
High quality sequence stop: 713.
High quality sequence stop: 713.
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Pred. No. 3.4e-19;
0; Mismatches 16; Indels
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                          1004 .
ACENCOURT_6541158 NIH_MGC_88 i
5', mRNA sequence.
BM555216
                                                                                                                                                   BM555216.1 GI:18795496
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Best Local Similarity 97.6%;
Matches 932; Conservative
                                                                                                                                                                                               Homo sapiens (human)
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/db_xref="taxon:9606"
//clone="InAGE:6302007"
//lab_bost="bH108 (phage-resistant)"
//clone_lib="NIH_MGC_113"
//clone_lib="NIH_MGC_11"
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0; Mismatches 20;
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Best Local Similarity 97.3%;
Matches 903; Conservative
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/lab_host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_li3"
/clone_lib="NIH_MGC_li3"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CADA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT_8484859 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6301179
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 915)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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780 AAAAATGCCTAAAGAACATCCACAGAATAGACCTGGAAGACAAAAATCCCGAAGTACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert stranders, First Benail: cgapbs-remail.nih.gov.
Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can intro-//image.lln.gov k column: 04
High quality sequence stop: 709.
High quality sequence stop: 709.
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Pred. No. 2.5e-18;
0; Mismatches 9;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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CAAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCA 1053
                                                                                                                              /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
//clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
//clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
//note="Ist strand cDNA was primed with a NotI-oligo(dI)
primer. Five prime end enriched, double-strand cDNA was
stingerted with Not I and cloned into the Not I and EcoR V
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSODC005BH08QP1.
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/db_xref="taxon:9606"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f Formore information about this cluster, see
                                                                                                                                                                                                                                                       AAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATC
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Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases I to 896)
LI,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/note="lat strand cDNA was primed with a NotI-oligo(dT)
/rote="lat strand cDNA was primed with Not I and cLoned into the Not I and ECOR V
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          CAAGCAGTCTGTTCAAGGAGCAGGGRCAAGTTACAGGAATGTTCTCCAAGCAGCAATCA 791
                                                                                                                                                                                                                                                                                                                                    on Feb 15, 2001 this sequence version replaced gi:12890528.
Contact: Genoscope contre National de Sequencage enerscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1297.f For more information about this cluster, see
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Catarrhini; Hominidae; Homo.
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cgi.bin/cluster.cgi?seq=cSoDIO60Ac06QPlecluster=1297.f. Contact
Feng Liang Email: filiang@lifetech.com/DR.:
http://fulllength.invitrogen.com/InvitroGen.Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO60Ac06QPI.
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Li,W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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STKGTTGAGTTGAR-----AAAYWAATTGGTGCCCARATCAATGGATTATAGAAAT 942
                                                                  CTGCCTGCTGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGGCTT 463
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NIH-MGC http://mgc.nci.nih.gov/.
523
                                                                                                                                                                                                        ACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCA 583
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                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCYAARRAMAYCMCAGAWAGACTKARACAAAATCMRARTACAGMGIYIKICAAG 996
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Contact: Robert Strausberg, Ph.D.
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Contact: Genoscope
Genoscope
Genoscope
Genoscope
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CS0CAP006CG04QPl&cluster=1297.f. Contact:
Feng Liang Email: fliang@lifetech.com/ RRL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0CAP006CG04QPl.
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/mol_type="mRNA"
/do_txref="taxon:9606"
/do_txref="taxon:9606"
/clone="CSOCAPO06XNO7"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCWNSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                                    CAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTT 1073
                                                                                                                                                                                                                                                                                                                               bp mRNA linear EST 22-MAY-2003
Homo sapiens cDNA clone CS0CAP006YN07
                                                          Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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Pred. No. 3.9e-16;
1; Mismatches 11;
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                                                                                                                                                                                                                                                                                                               902
BX457155 Homo sapiens THYMUS
5-PRIME, mRNA sequence.
BX457155
                                                                                                                                                                                                                                                                                                                                                                                                                                    BX457155.1 GI:31026861
                                                                                                                                         1074 CAAATAACTTCAGGCT 1089
                                                                                                                                                                  785 TCAATAACTTCAGGAT 800
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98.2%;
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Best Local Similarity 98.29
Matches 798; Conservative
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TITLE
JOURNAL
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                                                     1. .982.

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMMES:6284871"
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/clone_lib="hilb (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
RCORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size=selected >SOODp for average insert size into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >SOODp for average insert size i. 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
Library.

199 c 262 g 250 t lothers
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Pred. No. 2.1e-16;
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High quality sequence stop: 627, Location/Qualifiers
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al Similarity 98.5%;
784; Conservative
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/mol_type="mRNA"
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1 (Dases 1 to 1054)

S NIH-MGC http://mgc.nci.nih.gov/

IN Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inih.gov

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2025 row: 9 column: 04

High quality sequence start: 227

High quality sequence start: 227

High quality sequence start: 227

High quality sequence start: 227
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                         GAAGAAGCACTTGATACAGATGAGAAGAAGAGAGTGCTGCTTTTTGTGCGGGATGTTGCT
                                                                                                                                                                                                                               ATAGATGTGGTTCCACCTAATGTCAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAG
                                                                                                                                                                                                                                           GAAGAAGCACTTGATACAGATGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCT
             GGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGCAGGAGAGTCC
                                                        TGTCCTCATTAATTTTCCTCATGAAGGATTACA 839
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Homo sapiens
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/www.refe"taxon:9606"
/db.xrefe"taxon:9606"
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4.3e-16;
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Pred. No. 4.3e-
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Best Local Similarity 98.0%;
Matches 776; Conservative
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CD388330 900 bp mRNA linear EST 30-MAY-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmlOA70 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jamle Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                               480 CTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACA
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National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo saplens"
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High quality sequence stop: 646.
Location/Qualifiers
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mammary gland"
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i 173 c 230 g 191 t
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AU122196.1 GI:10937431
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Contact: Takao Isogai
Genomics Laboratory
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/note="Vector: pDONR201; Site_1: attP2; Site_2: attP1; LIBR_PRINTING - oligo dT; METHOD - full-length enriched; LIBR PROVIDER - Bradfield"
1 206 c 271 g 197 t
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                                          14; Length
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llarity 96.8%; Pred. No. 6.4e-15;
Conservative 0; Mismatches 19
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S NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

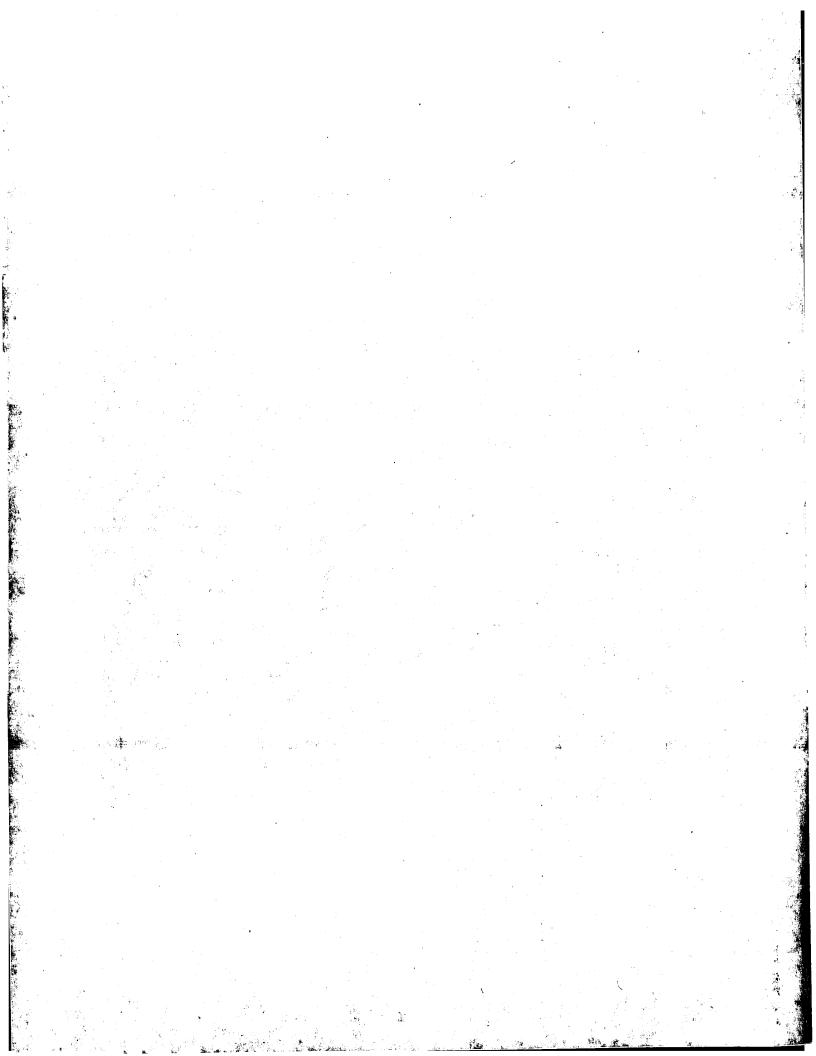
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13589 row: 1 column: 01
High quality sequence stop: 627.

Location/Cualifiers
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/note="vector: pCMV-SPORT6 (Life Technologies); Si
Noti: Site_2: Sali; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5/-TCGACCCACGCGTCGG-3' and
                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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/clone="IMAGE:6190608"
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Homo sapiens (human)
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Patent No. 6348573

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Nonez, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
                                       Sequence Sequence Sequence (
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US-09-591-992-1
US-09-23-878-5
US-09-340-6204-64
US-09-340-6204-63
US-08-131-629-8
US-09-11-150-3
US-09-759-359A-3
US-09-759-359A-3
US-09-758-894A-3
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99.0%; Pred. No. 0;
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Best Local Similarity 99.0
Matches 2003; Conservative
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	61 CCTGCTGGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCTTTGTGAGGTTCCC	67 TAGTCTAAGAGTAGGATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACA	27 GATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCT	87 AATGTCAGGGACCTTCTGGATATTTACGGGAAAGAGGTAAGCTGTCTGT	7 GCTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACTIIIIIIIIII	07 AGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTG	CTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTC	ATGAAGGATTACATGGGCCGAGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTG	7 GTTGAGTTGGGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAATGC 	CTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTT 	CAAGGACCAGGGACAAGTTACAGGAATGTTCTCCAAGGAGCAGTCCAAAAGAGTCTCAAGGIIIIIIIIII	GATCCTTCAAATAACTTCAGGCTCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAA 	CAGCTTGGCGCTCAACAAGAACCAGTGAAGAATCCATTCAGGAATCAGGAAGCTTTTTTG 	7 CCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCGAAGCCCCTAGGAATCTGCCTG 	247 ATAATCGATTGCATTGGCAATGACACAGAGCTTCTTCGAGACACCTTCACTTCCTGGGC	TAIGAAGTCCAGAAATICTIGGAICICAGTAIGGAIGGIAIAICCCAGAITCTIGGCCAA 	67 TTTGCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTG	27 GGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTC	7 ATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTT

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LENGTH: 2045 base pair
TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 1, Application US/08859167
Patent No. 6037461
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SALIGHT, Emad S.
APPLICANT:
FORD APPLICANT:
FORD APPLICANT:
FORD APPLICANT:
FORD AND APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
GENERAL OF INVENTION:
OF MAKING THE SAME
NUMBER OF SEQUENCES:
ADDRESSE:
ADDRESSE:
MOGGOCK, Washburn, Kurtz, Mackiewicz & No. 6037461ris
CITY:
CITY:
PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1619.2,
Pred. No. 0,
0; Mismatches
                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
FILING DATE:
CLASSIFICATION: 435
ATTOCHACY AGENT INFORMATION:
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-
TELECOMUNICATION INFORMATION:
TELECAMICATION INFORMATION:
TELEFAX: (215) 568-3100
                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                      WINDOWS
                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%;
llarity 94.1%;
Conservative
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Best Local Similarity
Matches 1747; Conserv
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                                                                                                                                                                                                     USA
                                                                                                                                                                                   STAIL.
COUNTRY: USE
19103
                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-859-167-1
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                                                                     106;
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                                          DB 3;
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                                          Score 1619.2;
                                                     Pred. No. 0;
0; Mismatches
                                          72.2%;
94.1%;
                                         Query Match 72.2
Best Local Similarity 94.1
Matches 1747; Conservative
 413..1750
  ; LOCATION:
US-09-109-273-1
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                                                                               1629 TGGAATTCAAGGCTCAGAAGCGAGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                          1395 CAGAGGCCAGCTGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATGAAGAATG
                                                                                             1455 TGGAATTCAAGGCTCAGAAGCGAGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCT
                            CAGAGGCCCAGCTGGAGAACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATGAAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTING DATE:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTING DATE:
NUMBER: DELUCATION:
NUMBER: DELUCATION:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleac acid
STRANDEDNESS: double
TOPOLOGY: both
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REFERENCE/DOCKET NUMBER: TJU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alnemri, Emad S. APPLICANT: Fernandez-Alnemri,
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Pred. No. 0;
0; Mismatches
                                                                                                   SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
                                                                                                                                     FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                               REJENENTION NORMER: TJU-
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.2%;
Best Local Similarity 94.1%;
Matches 1747; Conservative
                                        ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     413..1750
      Philadelphia
                                                                                                                                                                                                                                                                                                                           nucleic acid
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; LOCATION:
US-09-276-993-1
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                               COUNTRY:
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APPLICANT: Albemit, Emad S.
APPLICANT: Fernandez-Albemit, Teresa
TITLE OF INVENTION: FAND-LIRE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6207801ris
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One Liberty Place, 46th floor
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Patent No. 6207801
GENERAL INFORMATION:
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Patent No. 6576751

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Compositions For And Methods Of Making The Same

TITLE OF INVENTION: Compositions For And Methods Of Making The Same

FILLE REFERENCE: TUJ445

CURRENT APPLICATION NUMBER: US/09/723,450

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR FILING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

LENGTH: 1750
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                                                   GGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGT
                                                                                         ACATTGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAGGAGAAAT
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.1%;
Matches 1747; Conservative
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; LOCATION: (413)..(1750)
US-09-723-450-1
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US-09-723-450-1
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                                    TTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTACAGAGTGA
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429 GGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTG 4 1 1 1 1 1 1 1 1 1	CTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGAAGAGTGTCTCTCTC	TTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGACCTTCTGGATA	STAAGCTGTCTGTCGGGACTTGGCTGAACTGCTCTACAGAGTGA				849 GCAAGATAAGCAAGGACAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAACTAAATT 9 	909 IGGITGCCCCAGATCAACTGGATTIATTAGAAAATGCCTAAAGAACATCCACAGAATAG S 	969 ACCIGAAGACAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACA 1 	1029 GGAAIGITCICCAAGCAGCAATCCAAAAGAGTCTCAAGGAICCTTCAAAIAACTICAGGC 1 	1089 TCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAACAAGAAC 1	1149 CAGTGAAGAATCCAITCAGGAATCAGAAGCTTTTTGCCTCAGAGCATACCTGAAGAGA 1018	GATACAAGATGAAGAGCAAGCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATG	AGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATG CGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATTCTTGC 			CACTCAGGGCTCCCCTGCATCACATCAGGAGGATGTTCATGGGAGGCTIIIIIIIIII	
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                                                    STCTTGGAGGTGGATGGCCAGCGATGAAGAATG 1628
                                                                  CTCTTGGAGGTGGATGGGCCAGCGATGAAGAATG 1454
                                                                                                         CTGTGCACAGTTCACCGAGAAGCTGACTTCTTCT 1688
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INTRON: 6791-11583; INTRON:
11584-11675; 14539-14580
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40. 2.1e-42;
natches 65; Indels 12;
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2100 CAGITACTIGGGAGGCIGAGGIGGGAGGATCTITIGAACCCAGGAGITCAGGGTCAIAGC 2159
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                                                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
; OTHER INFORMATION: sequence for PEDF plus flanking sequences US-08-367-841A-43
                                                                                                             12;
                                                                   Score 175; DB 4; Length 22481;
Pred. No. 2.8e-42;
0; Mismatches 65; Indels 12
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REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTOMBY AGENT INFORMATION:
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ZIP: 10154
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
ADDIUM TYPE: Floppy Disk
POUTUM TYPE: Ploppy Disk
POUTUM TYPE: Ploppy Disk
                                                                     Query Match 7.8%;
Best Local Similarity 76.2%;
Matches 246; Conservative
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SOFTWARE: WORDPER!
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                                                                                          Sequence 43, Application US/08367841A

Patent No. 6119687

GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Redriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: DIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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OTHER INFORMATION: full length genomic
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. ADTH
REGISTARTION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 36434
REFERENCE/DOCKET NUMBER: 30264126US2
RELECPHONE: (212) 758-4800
TELECPHONE: (212) 751-6849
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                                                                                                                                                                                                                                                                                                                 2220 CCATCTCTTTAAAAAAAAAA 2242
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PIER TITLE OF INVENTION: DER TITLE OF INVENTION: DRG NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS:
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STATE: New York
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Fatent No. 6391850

GENERAL INFORMATION:
APPLICANT: No. 6391850 Bouck
APPLICANT: No. 6391850 Bouck
APPLICANT: No. 6391850 Bouck
APPLICANT: No. 6391850 Bouck
APPLICANT: Paul Gillis
TITLE OF INFORMATION NUMBER: US/09/875,223
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT APPLICATION NUMBER: US/09/875,223
FILE REFERENCE: 2020-2303
CURRENT FILING DATE: 1998-07-23
FRIOR APPLICATION NUMBER: US 09/122,079
FRIOR PILLING DATE: 1998-07-23
FRIOR APPLICATION NUMBER: US 08/899,304
FRIOR PILLING DATE: 1998-07-23
FRIOR PILLING DATE: US 08/899,304
FRIOR FILLING DATE: US 08/899,304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                     ; CTHER INFORMATION: full length genomic
CTHER INFORMATION: sequence for PEDF plus flanking sequences.
PGT-US95-07201-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.8%; Score 175; DB 5; Length 22481; Best Local Similarity 76.2%; Pred. No. 2.8e-42; Matches 246; Conservative 0; Mismatches 65; Indels 12.
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                                                      43:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                     LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                           NAME/KEY: Pl-147
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Unsure
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                                                                                                                                                                                                                                        FEATURE:
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APPLICANT: Stevens, Richard L.
APPLICANT: ATTACHAM, Shalom
TITLE OF INVENTION: HEMATOPOLETIC CELL SPECIFIC
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND USES
                                                                                                                                                                                                                    1921 ATAAGAAACCAAAAGGCTGGGCGTAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGG 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTTACTTGGGAGGTGAGGTGGGAGGATCTTTGAACCCAGGAGTTCAGGGTCATAGC 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2160 AIGCIGIGALTGIGCCTACGAATAGCCACTGCATACCAACCTGGGCAATATAGCAAGAIC 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9643 CAGCTACTTGGGAGGCTAAGGCAGGAGATCACTTGAATCCAGGAAGTGGAGGTTGCAGT 9584
                                                                                                                                                                                                                                              9763 CCGAGGGGGTAGATCACCTGAGGTCAGGAGTTTGAGACCATCCTGGCCAACATGGAGAA
                                                                                                                                                                                                                                                                                                                       1981 CCAAGGAGGCCAGATCACTTCAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGG-TAA
                                                                                                                                                                                                                                                                                                                                                                                                                                2040 ACGCTGTCCCTAGTAAAATGCAAAATTAGCTGGGTGTGGGTGTGGGTACCTGTGTTCC
                                                                                                                                                                    Gaps
                                                                                                                                                                    12;
                                                                                                              Length 22484;
                                                                                                                                                                 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,871
FILING DATE: 19920103
CLASSIFICATION DATE: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DAMBER: US/07/816,289
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DAMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US/07/635,544
FILING DATE: 13-JUL-1989
PRIOR APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1989
FILING DATE: 13-JUL-1989
FILING DATE: 13-JUL-1988
FILING DATE: US-DOS/MSTERIES US/07/224,035
FILING DATE: US-DOS/MSTERIES US/07/224,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
; LOCATION: 1...22484
; OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2
                                                                                                        7.8%; Score 175; DB 4;
76.2%; Pred. No. 2.8e-42;
tive 0; Mismatches 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCTCTTTAAAAAAAAAA 2242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TEANS
TITLE OF INVENTION: TRANS
TITLE OF INVENTION: THERE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steine, Kess
                                                                                                        Query Match
Best Local Similarity 76.24
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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--- CCAGCCTGGGCAACAAGCGAGACTCCATTTAAAAAAA 15923
                                                                                                                                                                                                                                                                                                                      1935 GCTGGGCGTAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCCAAGGAGGGCCAGA 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                1995 TCACTICAGGICAGGAGTICGAGACCAGCCIGGCCAACAIGGI-AAACGCTGICCCIAGI
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Sequence 7, Application US/08814095
Sequence 7, Application US/08814095
Sequence 7, Application Sequence 8
Sequence 7, Application Sequence 8
Sequence 
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
                                                                                                                                                                                                                                                                Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                      7.6%; Score 1/1.2,
76.8%; Pred. No. 4.2e-41;
+1ve 0; Mismatches 63
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ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMERY, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/POCKET NUMBER: 2391
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 35060 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                            Best Local Similarity 76.88
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15922 AAAAAACTAA 15913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2234 AAAAAAAAA 2243
                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3
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                SEQ ID NO 3
LENGTH: 24707
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                                                                                                                                                                                                   Query Match
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Patent No. 6485939
GENERAL INFORMATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001052
CURRENT APPLICATION NUMBER: US/09/740,027
CURRENT PILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2054 AAAAATGCAAAAATTACCTGGGTGTGGGTGGGTACCTGTGTTCCCAGTTACTTGGGAG 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2114 GCTGAGGTGGGAGGATCTTTGAACCCAGGAGTTCAGGGTCATAGCATGCTGTGATTGTG 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2174 CCTACGAATAGCCACTGCATACCAACCTGGGCAATATAGCAAGATCCCCATCTCTTAAAA 2233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1935 GGCTGGGCGTAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGAGGCAGA 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1995 TCACTICAGGICAGGAGITCGAGACCAGCCIGGCCAACAIGGI-AAACGCIGICCCIAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 7.8%; Score 174.8; DB 1; Best Local Similarity 77.7%; Pred. No. 2.7e-42; Matches 241; Conservative 0; Mismatches 57;
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.2830004
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)833-7533
TELEPHONE: (202)833-8716
INFORMATION FOR SEQ ID NO: 5.
SEQUENCE CHARACTERISTICS:
LENGTH: 17327 base pairs
TYPE: NUCLEIC ACID
STANDEDINESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
9745..16396
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16397..17327
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754..9596
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 621..753
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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; LOCATION:
US-07-906-871-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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FEATURE:

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LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /gene= "AR"
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
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NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
FEATURE:
NAME/KEY: exon
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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LOCATION: complement (29945..30073)
OCHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/EXE: exon
LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 11
FEATURE:
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: COMPLEMENT (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
                                                                                                                                                                                                                                                                       LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
NAME/KEY: exon
LOCATION: complement (34092..34358)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 2
                                                                                         FEATURE:
NAME/KEY: exon
LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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                                                                                                                                                                                                                                                     NAME/KEY: exon
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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RMATION: /function= "arsenite resistance waATION: gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 24090..25177
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
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COGATION: 4089.22464
OTHER INFORMATION: /standard_name= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /function= "non-translated'
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
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LOCATION: 25524..26009
IDENTFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 3
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LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence-EXPERIMENTAL
OTHER INFORMATION: /gene-"ACHE"
OTHER INFORMATION: /number-4
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IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" OTHER INFORMATION: /number= 6
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/number= 1
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28008..28129
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28129..28131
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27385..27387
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LOCATION: 22465..22537
       STRANDEDNESS: double
TOPOLOGY: linear
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FEATURE: NAME/KEY: LOCATION:

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Patent No. 6479269
GENERAL INFORMATION:
FOR THE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
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                                                              Length 72928;
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                                                                                                       0; Mismatches 127;
                                                                DB 3;
                                                              Score 169.8; DB 3 Pred. No. 2.1e-40;
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; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3
                                                              Query Match 7.6%;
Best Local Similarity 67.2%;
Matches 291; Conservative
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LENGTH: 174493
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US-09-009-913-1
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                                                                                                       Gaps
                                                              Score 170.6; DB 3; Length 35060;
Pred. No. 7.8e-41;
0; Mismatches 89; Indels 2;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2213 CAAGATCCCATCTTTTAAAAAAA 2239
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285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
/number- 16
                                                              7.68;
72.28;
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                       Matches 236; Conservative
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    ; OTHER INFORMATION:
US-08-814-095-7
                                                                                    Best Local Similarity
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CITY: Palo Alto
STATE: CA
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Search completed: August 22, 2003, 13:53:40 Job time : 153.706 secs

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August 22, 2003, 11:36:53; Search time 509.885 Seconds (without alignments) 9889.733 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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SUMMARIES

Description	flace 2 appropriate	Sequence 16. Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 34, Appl	Sequence 19, Appl	Sequence 5, Appli	Sequence 18, Appl	Sequence 1, Appli	Sequence 14, Appl	Sequence 26998, A	Seguence 37866, A	Sequence 24847, A	Sequence 35401, A	Sequence 35271, A	Sequence 23. Appl
QI	IIS-09-471-749-2	US-09-410-194-16	US-09-009-893-1	US-09-861-270-1	US-10-103-313-34	US-10-115-928-19	US-09-009-893-5	US-09-410-194-18	US-10-005-921-1	US-09-410-194-14	US-09-918-995-26998	US-09-918-995-37866	US-09-918-995-24847	US-09-918-995-35401	US-09-918-995-35271	US-09-009-893-23
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Score	2169.4	2124	2006.8	1952.2	1209.6	1209.6	9.668	849.6	813.6	731.8	431.4	423.2	419.4	382.4	345	313.4
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Sequence 436, Appl Sequence 25, Appl Sequence 26, Appl Sequence 3120, Ap Sequence 3120, Ap Sequence 1759, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 285441, Sequence 285441, Sequence 285440, Sequence 285441, Sequence 285441, Sequence 285441, Sequence 285441, Sequence 285441, Sequence 285441, Sequence 285441, Sequence 28641, Sequence 28641, Sequence 38641, Sequence 38641, Sequence 38691, Sequence 3448, Ap Sequence 3448, Ap Sequence 3448, Ap Sequence 3448, Ap Sequence 3448, Ap Sequence 2348, Appl Sequence 2348, Appl Sequence 3341, Ap	
US-09-833-381-436 US-09-009-893-25 US-09-009-893-24 SS-09-009-893-24 SS-09-009-893-24 US-09-009-893-24 US-09-864-761-3120 US-10-027-632-285441 US-10-027-632-285997 US-10-027-632-285997 US-10-027-632-28996 US-10-027-632-28996 US-10-027-632-28996 US-10-027-632-28996 US-10-027-632-28996 US-10-027-632-28996 US-10-027-632-9448	ALIGNMENTS 9 TOSIS ASSOCIATED PROTEINS Icals, Inc. 1,749 02 0519 US
490 10 US- 309 11 US- 309 11 US- 437 9 US-C 430 9 US-C 324 9 US-C 308 11 US- 389 10 US- 297 11 US- 527 13 US- 1912 13 US- 1913 13 US- 1914 10 US- 1915 13 US- 1916 13 US- 1917 9 US- 1918 13 US- 1918	17174 A1 A1 A1 APOP APOP 1100w 100w 1332 1332 100w 100w
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                                           Gaps
                                  1;
                             Length
                                  Indels
                             11;
                                  16;
                             8
                            Score 2169.4;
Pred. No. 0;
0; Mismatches
                             Query Match
Best Local Similarity 99.2%;
Matches 2190; Conservative
  pairs
 LENGTH: 2352 base pairs:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
LIBMADIATE SOURCE:
LIBMARY: THPIPLB02
CLONE: 157658
US-09-471-749-2
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	TTCCACCTAATGTCAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGT	ACCTIGTGGTTGAGTTGGAGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG 9	1119 TTAAGGAACAGCTTGACCAACAAGAACCAGTGAAGAATCCATTCAGGAATCAGAAG 178 1711
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	ESULT 2 S-09-410 Sequenc Patent GENERAL APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC	FILE REFERENCE: 11141-002001 CURRENT APPLICATION NUMER: U599-09-30 PRIOR APPLICATION NUMER: PCT/EP98/01857 PRIOR PLIING DATE: 1999-09-30 PRIOR FILING DATE: 1997-04-01 PRIOR FILING DATE: 1997-04-01 PRIOR FILING DATE: 1997-04-01 NUMBER: GERMANY 197 13 393.2 PRIOR FILING DATE: 1997-04-01 SOFTWARE: EastSEQ for Windows Version 4.0 SEQ ID NO 16 LENGTH: 2143 TYPE: DNA ONGANISM: Homo sapiens FEATURE: NAME/KEX: CDS LOCATION: (383)(1822) US-09-410-194-16	Query Match 94.7%; Score 2124; DB 9; Length 2143; Best Local Similarity 99.7%; Pred. No. 0; Matches 2138; Conservative 0; Mismatches 5; Indels 1; Gaps 1; Qy 99 TAGGGGGGCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/009,893 FILING DATE: HEREWITH
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches
                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 1-JAN-1997
PRIOR APPLICATION DATE: 0S 60/054,800
FILING DATE: 0S -40G-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2034 base pairs
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 1, Application No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NJ. USANA
APPLICANT: ROSEN, REINER L.
APPLICANT: RENEW JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APPLICANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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                                                               GAGACAAGAAAGAAAACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PT204C1
CURRENT APPLICATION NUMBER: US/10/115,928
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
53.9%; Score 1209.6;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1275; - Conservative 3; Mismatches
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| LOCATION: (1136)
| OTHER INFORMATION: n equals a,t,g, or c
US-10-115-928-19
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; Sequence 19, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFWARE: Patentin Ver. 2.0
SEQ ID NO 34
                                                                                                                                                                                                                           18; Indels
                                                                                                                                                                                                     DB 14;
                                                                                                                                                                                                   Score 1209.6;
Pred. No. 0;
3; Mismatches
                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: (1136)

: OTHER INFORMATION: n equals a,t,g, or c

US-10-103-313-34
                                                                                                                                                                                                   Query Match 53.9%;
Best Local Similarity 97.9%;
Matches 1275; Conservative 3
                                                                                                                    ORGANISM: Homo sapiens
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Sequence 5, Application US/0900993
Publication No. US20030087339A1
GENERAL INFORMATTON:
APPLICANT: NOSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: GENTZ, NISHVA M.
APPLICANT: GENTZ, SEINER L.
APPLICANT: GENTZ, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
1214 ACACCTGTGGTACCCAGCACTTTGGGAGGACCAAGGAGGCCAGATACACTTACAGGTCAG 1273
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                                               2009 GAGTTCGAGACCAG--CCTGGCCAACATGGTAAACGCTGTCCC 2049
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SOFTWARE PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTOMENY/AGENT INFORMATION:
ANALYMENT APPLICATION:
ANALYMENT OF THE PATENT OF THE PATE
                                                                     1274 GAGTTCGAGACCAGACCTGGACCAACATGGTAAACGCTGTACC
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Pred. No. 6.3e-
0; Mismatches
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REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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llarity 94.3%;
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2597 base naive
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS
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US-09-009-893-5
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                                                                                               ATTAGAAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTA
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Pred. No. 1.6e-247;
0; Mismatches 379;
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Sequence 1, Application US/10005921
Publication No. US20020174450A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINI
FILE REFERENCE: R-714
CURRENT APPLICATION NUMBER: US/10/005,921
CURRENT FILING DATE: 2001-12-04
PRIOR PELICATION NUMBER: US 60/254,902
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
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73.28;
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Best Local Similarity 73.2
Matches 1092; Conservative
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                                                                                                                                                                                         Score 731.8; DB 9;
Pred. No. 9.8e-222,
0; Mismatches 2;
                                     N
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EF98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 14
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Best Local Similarity 99.6%;
Matches 744; Conservative
                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (394)...(1056)
US-09-410-194-14
                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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 TTTTTTGCCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAAT
                                                                                                        GAGCCGAGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACGGGCTCCCCCT
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             CCTGGGCTATGAAGTCCAGAAATTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCT
                                                                                                                                           GCATCACATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAA
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APPLICANT: Thome, Margot
APPLICANT: Irmler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schroider, Pascal
APPLICANT: Schroider, Pascal
APPLICANT: Steiner, Veronique
APPLICANT: Steiner, Veronique
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROFEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: TSChopp, Jurg
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US-09-410-194-14
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Similarity 99.3%; Score 431.4; DB 11; Length 495;
Similarity 99.3%; Pred. No. 2.3e-126;
43; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37866, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
FULL OF INVENTION:
FULL OF INVENTION:
FOR VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                               APPLICANT: HYSIGATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OFFICE FILE PEPERALE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
SOFTWARE: FastERG for Windows Version 3.0
SEQ ID NO 26998
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                       Sequence 26998, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(495)
OTHER INFORMATION: n = A,T,C or G
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US-09-918-995-37866
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RESULT 11
US-09-918-995-26998
                                                                                                                                                                                                      ID NO 26998
ENGTH: 495
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Best Local Simi
Matches 443;
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1189 TCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGAT 1248
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                                                                                                                                                                                                                                          DB 11; Length 479;
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES

FILE REPERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.6%; Pred. No. 9.3e-124;
Matches 439; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24847
LENGTH: 479
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSSESEQ for Windows Version 3.0
SEQ ID NO 37866
LENGTH: 479
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                                                                                                                                                          NAME/KEY: misc_feature
LCCATION: (1)...(479)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-37866
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US-09-918-995-24847
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266 CTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAG 325
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                                                                                      TGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGC
                                                                                                                                                                                                                          278 TGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35271, Application US/09918995
; Publication No. US2003007362341
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; TITLE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
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LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C
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US-09-918-995-35271
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LENGTH: 443
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                                                                                                                                                                                        GCTTTTTTGCCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGA
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                                                                                      Gaps
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                                                    DB 11; Length 479;
                                                                                      Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARRE: FastERQ for Windows Version 3.0
SEQ ID NO 35401
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                                                    Score 419.4; DB 11;
Pred. No. 1.5e-122;
0; Mismatches 18;
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or
US-09-918-995-35401
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                                                Query Match 18.7%;
Best Local Similarity 95.9%;
Matches 440; Conservative
; OTHER INFORMATION: n - A,T,C US-09-918-995-24847
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LOCATION: (1)...(441)
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Matches 39
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Search completed: August 22, 2003, 17:24:07 Job.time: 519.885 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
<pre>Run on: August 22, 2003, 05:37:21 ; Search time 5123.69 Seconds</pre>
Title: Perfect score: 1373 Sequence: 1 ggacgtcgaggcattacaataaaaaaaaaaaaaaa
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% -Maximum Match 100% Listing first 45 summaries
Database : GenEmbl:* 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	A86558 Sequence 3 BD105909 CASH(Casp Y14040 Homo sapten A86556 Sequence 1 BD105908 CASH(Casp Y14040 Homo sapten AR194324 Sequence AR005774 Homo sapten AR005774 Homo sapten AR00516 Homo sapten AR00516 Homo sapten AR00516 Homo sapten AR00516 Homo sapten BD107658 FLIP gene U97074 Homo sapten A84918 Sequence 9 BD107658 FLIP gene U97075 Homo sapten A84918 Sequence 7 BD107659 FLIP gene BD107659 FLIP gene BD107659 FLIP gene BC001602 Homo sapten AR015450 Homo sapten AR015451 Homo sapten AR01559 FLIP gene BC029233 Mus musculu AR424166 Rattus musculu AR4424 Mus musculu X14042 Mus M	NA linear PAT 21-JAN-2000 EFFECTOR DOMAIN, MODULATORS OF
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/db_xref="taxon:32644"
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1373 bp DNA linear PAT 18-SEP-2002 CASH(Caspase Homologue) with death effector domain, modulators of ED105909
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DAVID WALLACH, TURA GOLTSEV, ANDREI KOVALENKO, EUGENE VARFOLOMEEV,
PI VADIM BRODIANEY
PC C12N15/12,C12N15/11,C12N9/64,A61K38/48,G01N33/68,C12N9/00 (Strandedness: Single;
PC TOPOLOGY: Linear;
PH Rey Location/Qualifiers.
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Patent: JP 2002500508-A 2 08-JAN-2002;
PED RESEARCH AND DEV CO LTD
PN JP 2002500508-A/2
PD 08-JAN-2002
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/mol_type="genomic DNA"
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GAGGCATTACAATCGCGAAACCAAGCCATAGCATGAAACAGCGAG 	TITILITIE III III III III III III III III III	121 CACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGAGGACCACG 180 	181 GGAGGAGGTGTAGGAGAGAGGCGCGGAACAGCGATCGCCCAGCACCAAGTCCGCTTCC 240 	241 AGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCCCCTTCCCGGGGTCTAGGGGAGGAA 300	301 GGCTGAGGTGGCGGCGGGGGGGGGGGGGGGGGGGGGGGG	361 GGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGCCTGC	421 TGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAG 480	481 GATGTCTGCAAGTCATCCATCAGTTGAAGAAGCACTTGATACAGATGAGAAGGAGAT 540 	541 GCTGCTCTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGACCT 600 	601 TCTGGATATTTACGGGAAAGAGGTAAGCTGTCTGTGGGGGACTTGGCTGAACTGCTCTA 660 	661 CAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGA 720 	721 GACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGAT 780 	781 IGGIGAGGATITGGATAAAUCIGAIGTGCTCATTAAITTTCCTCAIGAAGGATTACAT 840 	841 GGGCCGAGGCAAGATAAGCAAGAGAAGATTCTTGGACCTTGTGGTTGAGTTGGAGAA 900 	901 ACTAAATTIGGTGCCCGGATCAACTGGATTAATAGAAAAATGCCTAAAGAACATCCA 960 	961 CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTGTTGAAGGAGCAGGAC 	1021 AAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAA	1081 CTTCAGGATGATAACACCCTATGCCCATTGTCCTGATCTGAAAATTCT
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61 CTCACCGACGACTCTCAACTAAAAGGGACTCCCGGAGGTAGGGGTGGGGACTCGGCCTCA 120 121 CACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACCACCAACAACAACAACACGCGGG 121 CACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACACAACAACAACAACAACACGGGGTGGGGTGAGTGCCGCTTTGTCCAGTGACTGAC	GGCTGAGGTGGCAGCAGGAGGAGGCGCGCGAGGAGGACGAACTCCCCACTGGAAA GGCTGAGGTGGCAGCAGGAGGAGGCGCGCGGAGGAGGACCACTCGAAA GGCTGAGGTGGCAGCGGCAGGAGGAGCCGCCGCGACAGGACCACTCGAAA GGCTGAGGTGCAGCGGCAGGAGGAGCCCGCCGCAGGACCACTCCCCCACTGGAAA GGATTCTGAAAAAATGAAATCAGCCCTCAGAAATGAAGTTGACTGCCTGC	661 CAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGA 720 [1021 AAGTTAGAGAATGTTCTCCAAGCGACAACAAGAAGAAGAAGAAGAAGAAGAAGAAGA
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9
Location/Qualifiers

1. .2243
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
a 511 c 603 g 509 t
                                                                                     Score 1087.4; DB 6
Pred. No. 1.6e-206;
0; Mismatches 1;
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99.98;
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03-MAR-1998 JP 1998538331

03-MAR-1997 IL 120367,01-MAY-1997 IL 120759 PI

D WALLACH, YURA GOLFSEV, ANDREI KOVALENKO, EUGENE VARFOLOMEEV,

VADIM BRODIANSKI

C12N15/12,C12N15/11,C12N9/64,A61K38/48,G01N33/68,C12N9/00
                                                                                                                                                                                                                                                                                      CASH(Caspase Homologue) with death effector domain, modulators the function of FAS receptors Patent: JP 2002500508-A 1 08-JAN-2002; YEDA RESEARCH AND DEV CO LTD PN JP 2002500508-A/1
         GGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAA
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                                                                                     TCTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTA
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                                               GCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGGTTCCACCTAATGTCAGGGACCT
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JP 2002500508-A/1.
synthetic construct
synthetic construct
artificial sequences.
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Wallach, D., Goltsev, Y., Kovalenko, A., Varfolomeev, E. and
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PD 08-JAN-2002
PF 26-FEB-1998 JP 199
PR 03-MAR-1997 IL
DAVID WALLACH, YURA GOLT
PY VADIM BRODIANSKI
PC C12N15/12,C12N15/13
Strandedness: Single;
CC Topology: Linear;
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ACTABATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCA
                                                        AAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAA
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/product="CASH" alpha protein"
/product="CASH" alpha protein"
/product="CASH" also.1"
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RIDLKTKICKYROKYGONGGAFTSYRVUVQAAIOKSLEKINLVAPDQLDLLEKCLKNIH
RIDLKTKICKYROKYGONGGAFTSYRVUVQAAIOKSLEKINLVAPDQLDLLEKCLKNIH
RIDLKTKICKYROKYGONGGAFTSYRVUVQAAIOKSLECHILDETGREGLG
AQOEPVKKIGKIGOSONGGPRAMPRIDLIDGSPVCVLVSRGGSOSVTGVDOTHSGLICH
HIRNHMGDSCPYLAGKPRMFFIQNTVVSEGQLENSSLLEUG
CTVHREADFFWSTCATADMSLLEGSSHSSPSLTLQCLSQKLRQERRRPLLDLHIELNGYM
YDWNSRVSAKEKYYWLQHTLRKKLILLSYT"
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Submitted (23-700-1997) D. Wallach, The Weizmann Institute,
Department of Membrane Research & Biophysics, Rehovot 76100, ISRAEL
Location/Qualifiers
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                                                                      AAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAA 1080
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGAC
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CASH, a novel caspase homologue with death effector domain novel chem. 272 (32), 19641-19644 (1997)
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0; Mismatches 1;
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protein.
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CASH alpha

    .2243
    /organism="Homo :/mol_type="mRNA"

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HOMO Sapiens mRNA for CY14039
Y14039.1 GI:2653415
CASH alpha protein.
HOMO Sapiens (human)
HOMO Sapiens
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Best Local Similarity 99.9%;
Matches 1088; Conservative
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Wallach, D.
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2040 bp mRNA linear PRI 05-MAY-1998 Homo sapiens caspase-like apoptosis regulatory protein (clarp) AF005774
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RIDLKTKIQKYKQSVQGAGTSYRNVLQAAIQKSLKDSNNFRLHNGRSKEQRLKEQLG
AQQEPVKKSIQESEAFLDQSIPERRYKMKSKPLGICLIDCIGNETELLRDTFFTSLGY
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    Submitted (28-MAY-1997) Department of Pathology, University of Michigan Medical School, 1150 W. Medical Center Dr., C558 MSRBII, Ann Arbor, MI 48109, USA Location/Qualifiers
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                                                               ATGAAGGATTACATGGCCCGAGGCAAGATAAGCAAGGAGAAGATTTCTTGGACCTTGTG
                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosi
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases I to 2040)
Inohara,N., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
CLARF, a death effector domain-containing protein interacts or caspase-8 and regulates apoptosis
Proc. Natl. Acad. Sci. U.S.A. 94 (20), 10717-10722 (1997)
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Inohara,N., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
Direct Submission
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/note="CLARP; alternatively spliced"
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Unclassified.

Unclassified.

I (bases 1 to 2040)

RS Nunez,G., Inchara,N. and Koseki,T.

Compositions and methods for identifying apoptosis signaling pathway inhibitors and activators pathway inhibitors and activators

NAL Patent: US 634573-A 33 19-FEB-2002;

Location/Qualifiers

1. 2040

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Pred. No. 3.9e-194;
0; Mismatches 3;
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patent US 6242569.
                                                Unclassified.

1 (bases 1 to 2045)
Shu, H.-B. and Goeddel, D.V.
Regulators of apoptosis
Patent: US 6242569-A 1 05-JUN-
Location/Qualifiers
                                     GATCCTTCAAATAACTTCAGGAT 1089
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BD093439 117-AUG-2002 FADD-like anti-apoptotic molecules, methods of using the same, and compositions for and methods of making the same. BD093439.1 GI:22639027
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artificial sequences.
1 (bases 1 to 1750)
Alnemri, E.S.
FADD-like anti-apoptotic molecules, methods of using the same,
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181 GGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGG
                                                             549 TTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTTCTGGATA
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                                                                                                                          CTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAAGGAGGAGATGCTGCTCT
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Sequence 1 from patent US 6207801
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1 (bases 1 to 1750)
Alnemri, E.S.
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Strandedness: Double;
Topology: Both;
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Ositions for and methods of making the same nt: JP 2001527419-A 1 25-DEC-2001;
AS JEFFERSON UNIVERSITY
25-DEC-2001
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                                                                                                 Location/Qualifiers 413. .1750.
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                                              20-MAY-1998 JP 1998550515
20-MAY-1997 US 08/859167
                                                                                                                   Location/Qualifiers
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Best Local Similarity 99.5%;
Matches 1022; Conservative
                                                                  EMAD S ALNEMRI
       compositions
             Patent: JP 2
THOMAS JEFFE
PH 25-DEC-
PR 20-MAY-
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PI EMAD S
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CC STRANGE
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1 (bases 1 to 2056)
Srinivasula, S.M., Ahmad, M., Ottilie, S., Bullrich, F., Banks, S., Srinivasula, S.M., Ahmad, M., Ctilie, S., Bullrich, F., Banks, S., Armstrong, R.C. and Almemri, E.S., Framstrong, R.C. and Almemri, E.S., FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis
J. Biol. Chem. 272 (30), 18542-18545 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="anti-apoptotic molecule"
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to FADD, Moh4 and Mch5"
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848
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  789 ATTIGGATAAATCIGAIGIGCICCICATIAATTITCCICAIGAAGGATTACAIGGGCCGAG
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Alnemri, E.S.
Direct Submission
Submitted (18-JWN-1997) Microbiology and Immunology, Thomas, Jufferson University, Kimmel Cancer Institute, 233 S. Tenth, Street, Philadelphia, PA 19107, USA
Location/Qualifiers
1. 2056
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//MD_rref="mRNA"
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Homo sapiens FLAME-1 mRNA, complete cds.
AF009616
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413. .1750
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/map="2q33-34"
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CLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCV
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( pases 1 to 2039)

Shu, H.B., Halpin, D.R. and Goeddel, D.V.

Casper is a FADD- and caspase-related inducer of apoptosis Immunity 6 (6), 751-763 (1997)
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Pred. No. 7.3e-190;
0; Mismatches 2;
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Shu, H.B., Halpins, D.R. and Goeddel, D.V.
Direct Submission
Submitted (23-7UN-1997) Biology, Tulari
South San Francisco, CA 94080, USA
Location/Qualifiers
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TITICCTCATGAAGGATTACATGGGCCGAGCAAGATAAGCAAGGAGAAGAGTTTCTTGG 878
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Patent: WO 9844104-A 9 08-OCT-1998;
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schroeter, M. and Steiner, V.
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                                GAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTT
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 14 A84918

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JURG TSCHOPP,MARGOT THOME,KIMBERLY BURNS,MARTIN IRMLER,MICHAEL
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/organism='Homo sapiens, long version of
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Topology: Linear;
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11 Similarity 99.7%; Pred. No. 2.8e-184;
988; Conservative 0; Mismatches 2;
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/organism="unidentified"
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Sequence:

Scoring table:

2552756 seqs, 1349719017 residues IDENTITY_NUC Gaport 1.0 Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Human G1 protein 1	Human MACH related	. Human G1 protein i	Human apoptosis as	Human CLARP coding	Human MACH related	Human Casper gene.	Human FIN-1 encodi
SUMMAKIES		TD C		AAV52969	AAX25510	AAV52968	AA247926	AA248769	AAX25508	AAV50436	AAV31375
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	ф	Query Match		100.0	93.0	79.2	76.1	75.3	74.8	74.7	73.9
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AAV74136	AAD43202	AAV61937	AAZ39040	ABL52333	AAV44806	AAZ39041	ABL52332	AAV61936	ABK83474	AAZ56987	AAZ56989	AAZ56988	AAA54301	AAK73535	ABL52342	AAV61938	ABL52343	ABL52325	ABV72474	AAX25509	AAD16535	AAS34790	ABS64125	AAV44807	AAV46493	ABA4441	ABA54888	ABA24654	AAK03164	AAK28614	AAI13188	AAI34540	AAI03093	ABS28210	ABS03125	AAT21949
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73.5	73.5	71.1	71.1	71.1	62.7	62.5	62.5	62.3	59.9	53.9	44.0	44.0	44.0	29.7	27.2	27.2	24.6	24.6	24.6	23.7	23.6	23.6	23.6	23.6	22.7	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	14.3
1008.6	1008.6	975.8	975.8	975.8	860.8	858.2	858.2	855.4	823	739.8	604.8	604.8	604.8	408	373.8	373.8	337.8	337.8	337.8	324.8	324.4	324.4	324.4	324.4	311.4	276	276	276	276	276	276	276	276	276	276	196.2
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ALIGNMENTS

Gl protein; CASH-beta; human; caspase homologue; Fas receptor; modulator; apoptosis; cell death; inflammation; tumour; HIV; Human G1 protein isoform beta (CASH-beta) cDNA. AAV52969 standard; cDNA; 1373 BP. 11-JAN-1999 (first entry) therapy; ss. AAV52969; RESULT 1 AAV52969

Location/Qualifiers 482..1137 /*tag= a Homo sapiens Key

W09839435-A1

98WO-IL00098 26-FEB-1998; 11-SEP-1998,

971L-0120759. 971L-0120367. 01-MAY-1997; 03-MAR-1997; (YEDA) YEDA RES & DEV CO LTD.

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Varfolomeev

Kovalenko A,

Goltsev Y,

Brodianski V,

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WPI; 1998-495842/42.
P-PSDB; AAW78904.
 Wallach D;
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           useful
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This cDNA seqence codes for the beta isoform (see AAW78904) of novel human G1 protein. It was isolated from a human skin fibroblast corresponding to the G1 sequence. CC G1-beta (also called CASH beta, CASH being caspase homologue)

CG 1-beta (also called CASH beta, CASH being caspase homologue)

CG 1-beta (also called CASH beta, CASH being caspase homologue)

CG 4 and a longer isoform, G1-alpha (see AAW78903), represent 2 splice variants of the G1 protein. These G1 proteins are capable of binding to, or interacting directly or indirectly, with MORT-1

CC ASP-8), and thereby of binding to the intracellular domain of the FAS-R receptor, to which MORT-1 binds, or of binding to the intracellular domain of the p55 tumour necrosis factor (TNF)

CC ASP-8), and thereby of binding at the intracellular domain of the FAS-R receptor, to which TRADD binds and to which TRADD protein MORT-1 binds. Hence, they are considered as mediators or modulators of receptor, to which TRADD binds and to Which TRADD protein MORT-1 binds and to FAS-R, and also having a role in e.g. the signalling process that is initiated by the binding of FAS ligand to FAS-R, and also having a role in the signalling process initiated by the binding of FAS ligand (II), vectors and fragments are used to regulate cell death, and its inhibitors augment/enhance the processes. (II) and (III) requiate the FAS-R ligand or TNF effect on cells carrying an FAS-R or inflammatory processes. (II) is used to call searying an FAS-R or inflammatory processes. (II) is used to call searying an FAS-R or inflammatory processes. (II) is used to call searying an FAS-R or inflammatory processes. (II) is used to call searying an FAS-R or inflammatory processes. (II) is used to call searying an FAS-R or inflammatory processes. (III) is used to call searying an FAS-R or inflammatory processes. (II) is used to call searying an equation of its carrying a specific cell surface encoding (II), which kills the cell. Antisense or effects can also be regulated using a vector encoding a ribo DNA encoding isoforms of G1 protein which bind MORI-1 - and late the effects of FAS and tumour necrosis factor receptors, ful for killing of cells e.g. HIV and cancer cells Claim 4; Fig 2; 132pp; English

Sequence 1373 BP; 417 A; 283 C; 335 G; 338 T; 0 other;

ö 240 240 241 AGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAA 300 CACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGACCACG 180 180 9 CACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGACCAC GGAGGAGGTGTAGGAGAGAAGCGCCGCGAACAGCGATCGCCCAGCACCAAGTCCGCTTCC AGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGTTAGGGGGAGCGAA Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-222;
Matches 1373; Conservative 0; Mismatches 0; Indels 0; 241 301 301 361 181 -61 121 121 181 a ŏ g ò g δ g δy g å ò q ò

1260 1320 CATGTGATTAACATGGAACTGCCTCTACTTAATCATTCTGAATGATTAAATCGTTTCATT 1200 1200 960 096 900 900 840 480 480 540 540 9 900 999 99 720 720 GACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGAT 780 GGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAA GGGCCGAGGCAAGATAAGCAAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAA ACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCA CTTCAGGATGATAACACCCTATGCCCATTGTCCTGATCTGAAAATTCTTGGAAATTGTTC TTCTAAATGTGTTATAATGTGTTTTAGCCCTTTCTTGTTGCTGTATGTTTAGATGCTTTCC TGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAG GCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCT GCTGCTCTTTTGTGCCGGGATGTTGCTATAGATGTGGGTTCCACCTAATGTCAGGGACCT CAGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGA GATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGAT 1021 1081 1141 1261 1261 1321 1021 1081 1141 1201 1201 1321 961 541 661 721 721 781 781 841 841 901 901 196 541 661 421 361 g ò 셤 셤 ŏ g δ ద δŏ ò ద g ò g ŏ 셤 δý ద g ò 셤 à 셤 ò à 셤 g ð δ à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents DNA coding for MACH-related inducer of toxicity (MRIT) isoform MRIT beta 1 (see AAX'0578), a CED-4 homologue that has pro-apoptotic activity. An EST sequence having homologue that has pro-apoptotic activity. An EST sequence having homology to the p20 domain of human ICE-like protease MACHI/FLICE was isolated from an EST database. Several overlapping EST clones were sequenced to deduce the sequence of the full-length MRIT alpha 1 clone (see AAX25508) and beta 1 clone (see AAX25508) and 2 isoforms, alpha 2 (see AAX25509) and beta 2 in The MRIT gene was localised to the human chromosome 2432-33 and in the MRIT alpha 1. Selective enhancers and inhibitors of MRIT apparate of the full death of treat diseases proliferation. In addition, nucleic acid molecules encoding pro-apoptotic soforms of MRIT can also be used as inducers of pro-apoptotic isoforms of MRIT can also be used as inducers of pro-apoptotic soforms of MRIT can also be used as inducers of programmed cell death. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, angiogenesis and atherosclessis in treated by administering an agent that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selectively enhances MRIT apptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, Parkinson's disease, relinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 1308;
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                                            related inducer of toxicity MRIT beta 1 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying regulators of MACH-related inducer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1276.6; DB 20
Pred. No. 2.5e-206;
0; Mismatches 5;
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435..1100
/*tag= a
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99.5%;
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Matches 1290;
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              This cDNA seqence codes for the alpha isoform (see AAW78903) of novel human G1 protein. It was isolated from a skin fibroblast cDNA luman G1 protein. It was isolated from a skin fibroblast cDNA library using a cDNA probe corresponding to the G1 sequence.

G1-alpha (also called GASH alpha. CASH being caspase homologue) and a shorter isoform, G1-beta (see AAW78904), represent 2 splice variants of the G1 protein. These G1 proteins are capable of binding to, or interacting directly or indirectly, with MORT-1 or with MORT-binding proteins such as McA4 (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular domain of the FNS-R receptor, to which MORT-1 binds, or of binding to the intracellular domain of the p55 tumour necrosis factor (TNF) receptor, to which PRADD binds and to which TRADD protein MORT-1 binds. Hence, they are considered as mediators or medulators of 1 binds. Hence, they are considered as mediators or medulators of FAS-R having a role in e.g. the signalling process that is initiated by the binding of FAS ligand to FAS-R, and also having a role in the signalling process initiated by the binding of FAS ligand to FAS-R, and also having a role in the signalling process initiated by the binding of FAS ligand (II), vectors and fragments are used to regulate cell death, and its inhibitors augment/enhance the processes. (II) and (II) regulate the FAS-R ligand or TNF effect on processes. (I) and (II) regulate the FAS-R ligand or TNF effect on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate the effects of FAS and tumour necrosis factor receptors, useful for killing of cells e.g. HIV and cancer cells
                                                                                                                                                                                                                                                                                G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
modulator; apoptosis; cell death; inflammation; tumour; HIV;
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                                                                                    CTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1342
                                                                                                                                                                                                                                                        Human G1 protein isoform alpha (CASH-alpha) cDNA.
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Wallach D;
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482..1294
/*tag= a
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                                                                                                                                                                        AAV52968 standard; cDNA; 2243
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P-PSDB; AAW78903.
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cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other diseased cells can be treated using a viral vector encoding a viral surface protein, which binds a specific cell surface receptor and a sequence encoding (II), which kills the cell. Antisense oligonucleotides, introduced using the above vector, block the expression of (II) and can also requilate the above effects. These effects can also be requiated using a vector encoding a ribozyme that interacts with a cellular mRNA encoding (II), and allows (II)
                                                                                                                                                                                                DB 19; Length 2243;
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Pred. No. 1.9e-174;
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Best Local Similarity 99.9%;
Matches 1088; Conservative
                                                                                                                                     expression
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                                                                                                                       CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGAC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a human apoptosis associated protein designated HAPOP-1. HAPOP proteins are apoptosis regulators which have antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic activity. A pharmaceutical composition comprising HAPOP in conjunction with a carrier, a purified antagonist of HAPOP, vectors and agonists of HAPOP, are administered for diagnosing, treating or preventing disorders associated with increased or decreased apoptosis, e.g. cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as atherosolerosis, arteriosolerosis and cancers; immune disorders such as rheumatoid arthritis, systemic lupus erythematosus; reproductive disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as cirrhosis, colitis, hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins may be useful to detect and quantitate expression of HAPOP genes which are correlated with diseases and are also useful to detect differences
                                                                                                                                                                                                                                                                                                                                                     antlarteriosclerotic; antlarthritic; hepatotropic; apoptósis regulator; cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer; mmune disorder; rheumatoid arthritis; systemic lupus erythematosus; reproductive disorder; tumour; gastrointestinal disorder; cirrhosis; colitis; hepatitis; pancreatitis; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating or preventing disorders associated apoptosis -
         GGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAA
                                          CAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGAC
                                ACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCA
                                                                                                                                                                                                                                                                                                                                            Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn
                                                                                                                                                                                                                                                                                                                     Human apoptosis associated protein HAPOP-1 encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson
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                                                                                                                                                                                 Claim 7; Page 71-72;
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in the chromosomal location due to translocation, inversion etc., among normal, carrier, or affected individuals. The combination of the therapeutic agents may act syneagistically to effect the treatment or prevention of various disorders providing improved efficacy with lower dosages of each agent and thus reducing the potential for adverse side
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                                                                                                  BP; 652 A; 546 C; 628 G; 526 T; 0 other;
                                                                                                                             DB 21;
                                                                                                                             Score 1044.4; DB 21
Pred. No. 3.4e-167;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                      RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; cIDE-8; CIDE-8; DREP-1; diagnosis; cell growth; apoptosis dysregulation; enert therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
                                                                  GACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGT
                                                                                    CCCAGATCCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCACAGAATAGACCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases
                                                                                                                                   Example 10; Fig 2la; 93pp; English.
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                                                                                                                                                                                                                                                                                                                                                              Human CLARP coding sequence
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levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
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                                                                Sequence 2040 BP; 574 A; 467 C; 543 G; 456 T; 0 other;
                                                                                        Score 1033.4; DB 21
Pred. No. 2.4e-165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents DNA coding for MACH-related inducer of toxicity (MRIT) isoform MRIT alpha 1 (see AAV05787), a CED-4 homologue that interacts simultaneously with caspases and Bcl-2 family polypeptides, and which has pro-apoptotic activity. An EST sequence having homology to the p20 domain of human ICE-like protease MACH/FILEW as isolated from an EST database. Several overlapping EST clones were sequenced to deduce the sequence of the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see the full-length MRIT alpha 1 clone and 2 isoforms, alpha 2 (see the human chromosome 2q32-33 region. MRIT alpha 1 includes an N-terminal death effector domain and a C-terminal caspase homology channed death of systeine protease. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death. A cell accumulation disorder concoding pro-apoptotic isoforms of MRIT can also be used as inducers of programmed cell death. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, anglogenesis and atherosclerosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a
                            CAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAG
                                                                                                                                                                                                                                                                                                      MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; anglogenesis; atherosciencosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; aplastic ansemia; myocardial infarction; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying regulators of MACH-related inducer of toxicity
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                                                                                                    GATCCTTCAAATAACTTCAGGAT 1089
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neurodegenerative disorder, including Alzheimer's disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic
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                                                                                Sequence 1996 BP; 543 A; 461 C; 540 G; 451 T; 1 other
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Pred. No. 3.1e-164;
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                                CAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAG 1066
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identification of wild-type or mutant alleles, also in gene therapy to modulate expression of active Casper protein (using antisense or sense sequences). They are also used for recombinant production of Casper and to generate transgenic animals for testing candidate drugs for Casper-assoclated diseases.
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                                                                                                                                                                                                                                       caspase-eight-related protein; human; apoptosis; ds
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to identify specific modulators, identify or
sequences and in gene therapy
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P-PSDB; AAW69715.
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                 480 GGATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGA
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                                                         CAGGCTTTCGGTTTCTTTGCCTCCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes human FIN-1 (FLICE inhibitor-1), which is a caspase. FLICE (ICE-LAP7) is a protean of the interleukin-converting enzyme family, a protein involved in the regulariton of cell death. A host cell, comprising a vector containing FIN-1 encoding DNA, can be used to produce FIN-1. The vector containing the DNA can be used for producing a cell which expresses a polypeptide by transforming or transfecting the cell with it so that the cell expresses the polypeptide encoded the human cDNA contained in the vector. The polypeptide or its antagonist can be used in the treatment of patients needing FIN-1 by in-vivo administration. Conditions which may be treated include viral infection, tumours (especially solid tumours), ischaemic injury (e.g. stroke or myocardial infarction), neurodegenerative disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ACACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGGACAAGGACCAC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's or Parkinson's disease), osteoporosis, osteoarthritis, polycystic kidney disease, chronic degenerative liver disease, acquired immunodeficiency syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be used for chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED; apoptosis-related protein; caspase; viral infection; cancer; tumour; diagnosis; ischaemic injury; neuro-degenerative disorder; ds.
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422..1864
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                            AAV31375 standard; cDNA; 2188
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                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA sequence codes for human FLAME-1 (see AAW90107), or FADD-11ke apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic protein that interacts specifically with FADD, McD4, mcD4, mcD5 and FLAME-2. It is recruited to the Fas receptor complex and can abrogate Fas/TNF-induced apoptosis upon expression in Fas/TNF-induced apoptosis in Fas/TNF-induced apoptosis in tiself been generated from the Jurkat library using primers (see itself been generated from the Jurkat library using primers (see itself been generated from the Jurkat library using primers (see AAW84139-42) based on an isolated EST clone. Host cells, recombinant vectors, and methods of using FLAME-1 to identify substrates, activators or inhibitors of FLAME-1 are provided. FLAME-1, e.g. for treating HIV infection or Alzheiner's disease. Inhibitors of the polypeptides can be used as apoptotic agents. FLAME nucleic clidenciles can be used in vivo for antineoplastic purposes.
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                              FLANE-1; FADD-like apoptotic/anti-apoptotic molecule; human; apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy;
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          Human FLAME-1 cDNA.
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                                                 ATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATGGGCCGAG
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                                                                                                                                                                                                                            Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting apoptosis, treating diseases characterized by apoptosis e.g. HIV infection and Alzheimer's disease, and for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGACAACAAGGACCACGGGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGTCTCAACTAAAAGGGACTCCCGGAGCTAGGGGTGGGGACTCGGCCTCACACAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGGCTGAGG
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                                                                                                                                                                                                                                                                                               The invention relates to FADD-like apoptotic/anti-apoptotic proteins (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME sequences are useful for inhibiting apoptosis and for gene therapy of diseases characterised by apoptosis including HIV infection and Alzhelmer's disease. FLAME inhibitors are useful as apported apoptotic agents and activators are useful as anti-apoptotic agents. FLAME-1 is useful as a substrate for caspase in assays to identify caspase inhibitors. The present sequence is human FLAME-1 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Score 1008.6; DB 24; Length 1750;
Pred. No. 3.6e-161;
0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1750 BP; 465 A; 400 C; 476 G; 409 T; 0 other;
                                     "Human FLAME-1 protein"
        Location/Qualifiers
413..1750
/*tag= a
                                                                                                                                                                                                                                                                             Claim 7; Page 12-14; 35pp; English.
                                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.5%;
Best Local Similarity 99.5%;
Matches 1022; Conservative
                                                                                                                 28-OCT-1997; 97US-0959167.
26-MAR-1999; 99US-0276993.
28-NOV-2000; 2000US-0723450.
                                                                                                2001US-0935223
                                     /product-
                                                                                                                                                                                               WPI; 2002-642259/69.
P-PSDB; AAE26086.
                                                        US2002086983-A1
                                                                                                22-AUG-2001;
                                                                                                                                                                                                                                                           the protein
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AGTCTGTTCAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGA 1058
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                                                                      AAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGC
                    ACCTTGTGGTTGAGTTGGAGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
383..1825
**Atag= a**
/product= "FLICE-like inhibitory protein long form"
/note= "FLIP-L; apoptosis inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                   Human FLICE-like inhibitory protein long form nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating conditions characterized by vascular wall inflammation
                                                                                                                                                                                                                                                                                                                                                                                                       Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S; FLICE-like inhibitory protein short form; apoptosis inhibitor; arteriosclerosis; vascular wall inflammation; vascular injury; Fas ligand-mediated apoptosis; atherosclerosis; transplant; ss.
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P-PSDB; AAY57454.
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                                                                                                                                                                                        This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and
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                                    Hahne M, Hoffmann K;
P, Schroeter M, Steiner
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Pred. No. 1.2e-155;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                        Sequence 2143 BP; 589 A; 482 C; 576 G; 495 T; 1 other;
                                                                                                                           product
                                                                                                                              gene
                                                                                                                            New DNA encoding for anti-apoptotic infections and autoimmune diseases
                                     French EL, H
, Schneider F
Hofmann K;
                                                                                                                                                                  Claim 20; Fig 4B; 45pp; German
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Local Similarity 99.7%;
hes 988; Conservative
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                                     Burns K,
Rimoldi D
                                                                 Tschopp J,
                                                                                     WPI; 1998-532710/46.
P-PSDB; AAW76631.
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(TSCH/) TSCHOPP J. (APOT-) APOTECH SA.
                                       Bodmer J,
Irmler M,
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                                                                                                   TCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGCGAGGAGAGTCCGGCCGCGACA
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 Length 2143;
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             Indels
20;
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DB
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Score 975.8;
Pred. No. 1.3
71.18;
99.78;
            988; Conservative
      Similarity
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The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule (II) encoding a natural dominant negative regulator of cases 8, Filp-C, where (I) specifically pridises with and inhibits expression of the protein, or specifically hybridises with at least an 8-nucleobase portion of an active site on thibitor of Filp-C expression, a modulator of apoptosis and can be used inhibitor of Filp-C expression, a modulator of apoptosis and can be used in antisense gene therapy. (I) is useful for inhibiting the expression of Filp-C in cells or tissues, and for traating an animal having a disease or condition associated with Filp-C. (I) is also useful for modulating apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or caspase 7 is activated, and the Filp-C. (I) is also useful for diagnostics, therapeutics, prophylaxis, as research caspants and kits, for distinguishing functions of various members of a blological pathway, and in antisense gene therapy. (I) is also useful cormiton. The prevent or delay infection, inflammation or committee formation. The prevent sequence encodes human FLP-C as given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
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                                                                                                                          Human, FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
phosphorothioate; antisense modulation; infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAGGGGTGGGGACTCGGCCTCACACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 975.8; DB 24
Pred. No. 1.2e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                             encoding cDNA SEQ ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
383..1825
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99.78;
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(first entry)
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P-PSDB; ABB09294.
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Best Local Similarity
                                                                                                                                                                                                                                tumour; gene; ss.
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                                                                    Human FLIP-c
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15-JUL-2002
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I-FLICE-1 coding sequence.

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                                           TCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAGTCCGGCCGCGACA 338
                                                                                                                                                                                                                                                                                                780 ACCITGIGGITGAGITGGAGAAACTAAAICIGGITGCCCCAGAICAACIGGAITIAITAG
                                                                                                                                                                                                                                                                                                                               879 ACCTIGIGGTIGAGTIGGAGAAACTAAATTIGGTIGCCCCAGATCAACTGGATTTAITAG
                                                                                                              GGACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAA
                                                                                                                                      TTGATACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGG
                                                                                                                                           AGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACT
                                                                                                                                                                                                              TITICCICATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGG
     AGCTGAGACAACAAGGACCACGGGAGGAGGTGTAGGAGAAGAAGCGCCGCGAACAGCGATC
                     GCCCAGCACCAAGTCCGCTTCCAGGCTTTCGGTTTGCCTCCATCTTGGGTGCGCCT
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This sequence encodes an inhibitor of of Fas-ligand associated with death domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The proteins can inhibit both TWFR-1 and CD-95 induced apoptosis. These are the first examples of a naturally occurring catalytically inactive cappase that can act as a dominant negative inhibitor of apoptosis. The case that can act as a dominant negative inhibitor of apoptosis. The polypeptides and agonists can be used for treating e.g. Alzheimer's can stocke. CNS inflammation, osteoporosis, ischaemia, repertusion injury, call death associated with cardiovascular disease, polycystic kidney disease, apoptosis of endothelial cells in cardiovascular disease, cardionas in cardiovascular disease, cardiomas, carcinomas with p53 mutations, damage. Antagonists of the polypeptides can be used for treating cancers consummed adependent tumours, and cancers of the breast, ovary, prostate, bone, liver, lung, pancreas, and spleen), autoimmune disorders con remunatoid arthritis), and viral infections (e.g. theumatoid arthritis) and viral infections (e.g. therpse viruses, occur graft rejection, and chronic graft rejection. The products can also be used for detection, diagnosis and drug screening.
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                                                      FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 CGATCGCCCAGCACCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2034 BP; 560 A; 456 C; 540 G; 478 T; 0 other;
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                                                                                                                                                                                                                         Location/Qualifiers
268..1710
/*tag= a
                                                                                                                                                                                                                                                                         /*tag= a
/product= I-FLICE-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI INC
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97US-0034205.
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(UNMI ) UNIV MICHIGAN.
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21-JAN-1997;
                                                                                                                                                                                          Homo sapiens
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Best Local Si
Matches 873;
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                                                             I-FLICE-1;
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AAV44806 standard; DNA; 2034

RESULT 14 AAV44806

(first entry)

16-0CT-1998

AAV44806

SXXXE

Mon Aug

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The present sequence encodes human FLICE-like inhibitory protein short form, designated FLIP-S. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FLIP molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                     GAACTCCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                           ACTGCCTGCTGGCTTT-CTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCT
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            form.
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                                                                                                                                                                                                                                                                                                                  62.5%; Score 858.2; DB 20; Length 1062; llarity 99.5%; Pred. No. 7.6e-136; Conservative 0; Mismatches 3; Indels 1;
            short
/*tag= a
/product= "FLICE-like inhibitory protein
/note= "FLIP-S; apoptosis inhibitor"
                                                                                                                                                                                                                                                                                                 Sequence 1062 BP; 328 A; 212 C; 246 G; 276 T; 0 other;
                                                                                                                  BOSTON INC
                                                                                                                                                                                  conditions characterized by
                                                                                                                  CENT
                                                                                                                                                                                                      English
                                                                                                                 ELIZABETH'S MEDICAL
                                                                                              98US-0075471
                                                                                                                                                                                                    Example 2; Page 71; 105pp;
                                                                                                                                                      WPI; 1999-527469/44.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 871; Conserv
                                                                                                                                                                P-PSDB; AAY57455
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                                      W09942570-A1
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                                                                                                                                                             TGTGGTTCCACCTAATGTCAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAGCTGTC
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                                              ATGAAGTTGACTGCCTGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human FLICE-like inhibitory protein short form nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S; FLIP-S; FLICE-like inhibitory protein Short form; apoptosis inhibitor; arteriosclerosis; vascular wall inflammation; vascular injury; Fas ligand-mediated apoptosis; atherosclerosis; transplant; ss.
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Search completed: August 22, 2003, 07:51:31 Job time : 383.562 secs

BM555216 AGENCOURT

Run on:

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AL526318 1071 bp mRNA 11near EST 23-MAY-2003
AL526318 Homo sapiens NEUROBLASTOMA COT 25-NORWALIZED Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Feb 13, 2001 this sequence version replaced gi:12789811.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
MCHEP://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODCO16BH03QPlscluster=1297.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
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B0898388
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BX353373 BX353373
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                                                                                                     August 22, 2003, 07:06:39; Search time 3003.82 Seconds (without alignments) 11109.213 Million cell updates/sec
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             GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                               nucleic search, using sw model
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Database

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ALIGNMENTS

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digested with Not I and cloned into the Not I and EcoR y
sites of the pcMyspORT 6 vector. Library was normalized."

228 c 295 g 244 t 8 others
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InVitroGen Corporation 1600 ID : CSODC016BH03QP1.
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                                                                                                                                       Length 1071;
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                                                                                                                                        Score 973.2; DB 9;
Pred. No. 2.4e-76;
2; Mismatches 5;
  http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualiflers
                                                                                                                                          70.98;
99.28;
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into EcoRI; cDNA made by oligo-dT priming. Directionally cloned
GGCACGAG(G). Size=selected >500bp for average insert size
GGCACGAG(G). Size=selected >500bp for average insert size
GGCACGAG(G). Size=selected by Ling Hong in the laboratory
of Gerald M. Rubin (University of Callifornia, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Homo sapiens CDNA clone IMAGE:5798043
                                                                                                 AAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAG 1000
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NHF-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2025 row: g column: 04
High quality sequence start: 227
High quality sequence stop: 376.
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/db_xref="taxon:9606"
/clone="IMAGE:5798043"
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AGENCOURT_6703484 NIH_MGC_100
5', mRNA sequence.
BM928334
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976; Conserv
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us-09-380-546a-3.rst

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Contact: Genoscope

Contact: Genoscope

Genoscope - Centra National de Sequencage

BP 191 91006 EVRY cedex - France

Invariance on This sequence belongs to sequence cluster 1297.f For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq-cS0DC005BH0BQPl&cluster=1297.f. Contact:

Feng Liang Emall: fliangelifetech.com URL:

Franday Avenue Genoscope sequence ID: CS0DC005BH0BQPl.

Location/Qualifiers
  sapiens
                                                                                                                                                                                                                                                                                                                                                /MLX_LYEF= minns
/MLX_LYEF= minns
/db_xref="taxnon:9606"
/clone="CSODCO05YO16"
/clasue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="thono sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

a 184 c 238 g 219 t 4 others
                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 7.2e-67;
4; Mismatches 4; Indels 1:
BX353373 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED CDNA clone CSODC005YO16 5-PRIME, mRNA sequence. BX353373
                                                                                                                       and Polayes, D. I normalization
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/mol_type="mRNA"
                                                                                                      1 (bases 1 to 896)
Li,W.B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
Unpublished
                                  BX353373.1 GI:30383781
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Best Local Similarity 99.0%;
Matches 876; Conservative
                                                           Homo sapiens (human)
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          TCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAG
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Superscript II RT (Life Technologies). Note: this is NIH MGC Library." 220 t 1 others
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contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov ocolumn: 08
High quality sequence stop: 669.
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I. coation/Qualifiers
irce //ob_rref="marka"
//do_type="mRNA"
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//do_type="mRNA"
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//lab_host="DHIOB (phage-resistant)"
//lab_host="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2:
//note="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2:
//note="Organ: spleen; Vector: poTB7; Library constructed by Ling Hong in the
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT_7975998 NIH_MCC_113 Homo sapiens CDNA clone IMAGE:6214879 5', mRNA sequence.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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927 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8495301 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302007
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BQ712545
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov m column: 16
High quality sequence start: 4
High quality sequence stop: 632.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:550264"
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Technologies. Note: this is a NIH_MGC Library.
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291 q 228 t 4 others
                AGENCOURT_6541158 NIH_MCC_88 Homo sapiens cDNA clone IMAGE:5550264 5', mRNA sequence.
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NIH-WGC http://mgc.noi.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM12262 row, column: 01
High quality sequence stop: 713.
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Pred. No. 3e-66;
0; Mismatches 16; Indels 7;
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 97.6%;
Matches 932; Conservative (
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0; Mismatches 20;
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11 Similarity 97.3%;
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                                                                        CAGTCTGTTCAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAAT-CCAAAA 1056
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<u>AAAAATGCCTAAAGAACATCCACAGAATAGACCTGGAAGACAAAAATCCCGAAGTACAAG</u>
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Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM516 row: k column: 04
High quality sequence stop: 709.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 9.2e-64;
0; Mismatches 25
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http://image.llnl.gov
Plate: LLCM2483 row: c colu
High quality sequence stop: 6
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   CCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGT
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian
Unpublished
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Onpublished
On Feb 15, 2001 this sequence version replaced gi:12890528. Contact: Genoscope
838 IGCIGGCITI-CIGTIGACIGGCCCGGRGCIGIACIGCAAGACCCTIGIGAGCIYCCCIA 780
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns for sequence cluster, see
http://www.genoscope.cns.fr/
cgi-binColuster.cgi-Stoge-CS0DC005BH08NP1&cluster=1297.f. Contact :
Feng Liang Email: fliang@llfetech.com URL :
Feng Liang Email: fliang@llfetech.com VRL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC005BH08NP1.
                                                                                                                                                                                                                                                                                                                    BX353372 Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC005YO16 3-PRIME, MRNA sequence.
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                                                                                                                                                                 /tissue_type="NEUROBIASTOMA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pckWSPORT 6 vector. Library was normalized."
213 c 172 g 193 t 104 others
                                                     CAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTT 1073
                                                                                                            .074 CAAATAACTICAGGATGATAACACCCTATG-CCCATTGTCCTGATCTGAAAATTCTTGGA 1132
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases: 1 to 898)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
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          DB 13; Length 898;
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85.2%; Pred. No. 2.6e-60;
:1ve 99; Mismatches 32; Indels
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NIH-WGC http://mgc.nol.nlh.gov/.
                                 884 GTGGTTGAGTTGGAGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAA
                                                                                                                                                                                                                               824 CICATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can |
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
trow: f column: 16
High quality sequence stop: 514.
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prinner. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized."
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-cSOD1060Ac066plscluster=1297.f. Contact :
Feng Libra Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1060Ac066pl.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.N.A.G.E. Consortium/LINIX at:
www-bio.llnl.gov/bbrp/Aimage/Aimage.html
Insert Length: 1238 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
           Homo sapiens (human)
                       Homo sapiens
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                                                                                                             GCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATG
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                                                   DB 13; Length 839;
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   NIH_MGC Library."
235 t 4 other
                                                                           32;
                                                  Score 774.2; DB 1
Pred. No. 5.4e-59;
0; Mismatches 32
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      this
200
                                                     56.4%;
96.1%;
       NIH). Note:
153 c
                                                              Best Local Similarity ... Matches 791; Conservative
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/clone="IMAGE:1927372" /tissue_type="adenocarcinoma" /lab_host="DH10B"

/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

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781
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                                                                                                                                      ATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATG
                                                                                                                                                CTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTT
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                                                                                                                      3;
                                                                                                      Length 826;
                                                                                                                      13; Indels
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6
                                                                                                    Score 772.8; DB 9
Pred. No. 7.2e-59;
0; Mismatches 13
                                                                                                       Query Match 56.3%;
Best Local Similarity 98.1%;
Matches 813; Conservative
                                                                                243
                                                                                                                                                                                                                                                                                                                  782
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o e do de la completación de la

gp60a03.x1 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1927372 3' similar to TR:015138 015138 CASPASE-LIKE APOPTOSIS REGULATORY PROTEIN 2. [1]; , mRNA sequence.

GI:4084259

AI347041 AI347041.1

ACCESSION VERSION

LOCUS AI347041/c

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linear EST 01-AUG-2002
MAMMA1001850 5', mRNA
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                                                                                                                                     GGTGCGCCTTCCCGGCGTCTAGGGGAGCGAGGCTGAGGTGGCAGGAGGAGTCC
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                                                                                CAAGCCATAGCATGAAACAGCGAGCTTGCAGCCTCACCGACGAGTCTCAACTAAAAGGGA
                                                                                                                                                                                                                                                                                                                                                            509 GAAGAAGCACTIGATACAGAIGAGAAGGAGAIGCIGCICTITITIGIGCCGGGAIGTIGCI
                                                       Gaps
                                                       3;
                                                     Indels
                              Length
                            Score 759; DB 13;
Pred. No. 1.1e-57;
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                                                     1; Mismatches
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                            55.3%;
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Homo sapiens
                                        1 Similarity 98.2
798; Conservative
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AU122196
AU122196.1
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Matches 798
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/mol_type="mRNA"
/do_tref="taxon:9606"
/dlone="CSOGAPO065W7"
/tissue_type="THYMUS"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a Noti-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX457155
BX457155 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP006YN07 5-PRIME, mRNA sequence.
BX457155.1 GI:31026861
                                                                                1021
                                                                                                                                 1082 TTCAGGATGATAACACCCTATGCCCATTGTCCTGATCTGAAATTCTTGGAAATTGTTCC 1141
                                                                                                                                                                                                                                                                                                   TCTAAATGTGTTATAATGTGTTTTAGCCCTTTCTTGTTGCTGTATGTTTAGATGCTTTCCA 1261
                                                                                                                                                                                                                                            1142 ATGTGATTAACATGGAACTGCCTCTACTTAATCATTCTGAATGATTAAATGGTTTCATTT 1201
                                                                                                        290
                                                                                                                                                                                                                 229 TTCAGGATGATAACACCCTATGCCCATTGTCCTGAAAATTCTTGGAAATTGTTCC 170
                                                                                                                                                                                                                                                          GGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAA 410
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                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY codex - France
Bmall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1297.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAPO06CG040Plscluster=1297.f. Contact
Feng Liang Email : fliangellifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO06CG04QPl.
                                                                                                                                                                                                                                                                                                                 CTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCAC
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AUTHORS
TITLE
JOURNAL
COMMENT
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BX457155
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KEYWORDS
SOURCE
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CD38B330 900 bp mRNA linear EST 30-MAY-2003
AGENCOURT_14286562 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
CD38B330
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                                             944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 900)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Vector: pDONR201; Site_1: attp2; Site_2: attp1;
LIBR_PRIMING - oligo dr: METHOD - full-length enriched:
LIBR_PROVIDER - Bradfleld"
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                                                                                                                                       TGAAGGATTACATGGG-CCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGA-CCTTGT
                                                                                                                                                            886 GGTTGAGTTGGAGAAACTAAATTTGG-TTGCCCCAGATCAACTGGATTTATTAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Gina Zastrow-Hayes CDNA Library Preparation: Gina Zastrow-Hayes CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDKM77 row: 1 column: 09 High quality sequence start: 29 High quality sequence start: 29 High quality sequence Stop: 646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda. MD 20892
Email: capabs-remail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%; Score 719.6; DB 14; 96.8%; Pred. No. 2.9e-54; iive 0; Mismatches 19;
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/tissue_type="Trophoblast"
/lab_host="DH10B TonA"

    .900
    /organism="Homo_sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD388330.1 GI:31226484
                                                                                                                                                                                                                                                                                                                              945 GCCTAAAGAACATC 958
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Homo sapiens
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Best Local Similarity 96.8
Matches 767; Conservative
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CD388330
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3975
Fax: 81-438-52-3976
                Vertebrata; Euteleostomi;
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Pred. No. 1.6e-55;
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/clone_lib="MAMMA1"
/note="Vector: pME18SFL3"
173 c 230 g 191 t
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/clone="MAMMA1001850"
                Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 795)
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: ./cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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	Description	Sequence 33, Appl	7,7	Sequence 1, Appl1	٦,	-	Sequence 1, Appli	10	12,	7,7	13	89	63,	24,	99	73,	ų	Sequence 1, Appli	Sequence 1, Appli	36	'n	'n	Sequence 64, Appl	'n	33	Patent No. 5498694	Sequence 39, Appl	Sequence 15, Appl
SUMMARIES .	D	US-09-069-023-33	US-08-795-088A-1	US-08-859-167-1	US-09-109-273-1	US-09-276-993-1	US-09-723-450-1	US-08-545-196B-10	US-08-545-196B-12	US-08-909-965C-7	US-09-372-422A-19	US-09-489-847-89	US-08-821-994-63	US-09-149-476-24	US-09-904-615-66	US-09-461-325-73	US-09-013-810-1	US-09-234-245-1	US-09-328-965-1	US-09-461-325-36	US-09-027-137-2	US-09-344-441-2	US-09-489-847-64	US-07-867-106-2	US-09-247-373B-33	5498694-3	US-09-372-422A-39	US-09-152-060-15
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	Score	1033.4	1025.2	1008.6	1008.6	1008.6	1008.6	79.4	79.4	78.4	78	77.8	76.8	75.6	75.2	75	74.8	74.6	74.4	74.4	74.2	74.2	74	73.2	72.8	72.6	72.6	72.2
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Sequence 10, Appl Sequence 95, Appl Sequence 59, Appl Sequence 27, Appl Sequence 17, Appl Sequence 17, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 1, A	IDENTIFYING APOPTOSIS AND ACTIVATORS	•	AGCGAGCTTGCAGCCTCACCACGAGTCTCAACTAAAAGGGACTCCCGGAGCTAGGGGTG 106 	GGGACTCGGCCTCACAGTGAGTGCCGGCTATTGGACTTTTGTCCAGTGACGCTGAGA 166 	CAACAAGGACCACGGGAGGAGGTGTAGGAGAGAGCGCCGCAACAGCGGTCGCCCAGCA 226 	CCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCG 286	TCTAGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGATCCGGCCGCGACAGGACGAAC 346 		CCTGCTGCTGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCC 466
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28 30 30 31 31 31 31 31 31 31 31 31 31 31 31 31	RESULT 1 US-09-069-023-33 Sequence 33, Applic. Patent No. 634873 GENERAL INFORMATION APPLICANT: INODATA APPLICANT: INODATA APPLICANT: INODATA TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION CURRENT FILING DAT CURRENT FILING DAT NUMBER OF SEQ ID N SOFTWARE: PATENTIN SEQ ID NO 33 LENGTH: 2040 TYPE: DNA ORGANISM: HOMO SA US-09-069-023-33	Query Best Match	OY 47	Qy 107 Db 61	Qy 167 Db 121	Qy 227 Db 181	Qy 287 Db 241	Oy 347 Db 301	Qy 407

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107

227 257 287 317 347 377

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CCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAAATGAAGTTGACTGC 407
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Pred. No. 1.7e-226;
0; Mismatches 3;
 ATOMNET Geman, Richard A REGISTRATION NUMBER: 36,627
REFERENCE/FOCKET WUMBER: 197-001
TELECOMMUTCATION INFORMATION:
TELEPHONE: (650) 343-434
TELEFAX: (650) 343-434
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2045 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ilarity 99.6%;
Conservative (
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US-08-795-088A-1
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Best Local Similarity
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Patent No. 6242569
GENERAL INFORMATION:
APPLICANT: Sul, Hong-Bing
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: Regulators of Apx
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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	leation US/08859167 51 TION: TION: TION: THE BAD S. THE SAD S. THE SAD S. THE SAD S. THE SAME AND COMPOSITIONS FOR AND METHODS OF MATION: THE SAME AND COMPOSITIONS FOR AND METHODS THE SAME THE S	19103 1 TYPE: FLOPPY disk TYPE: FLOPPY disk TER: IBM PC compatible THE SYSTEM: WINDOWS TH	%; Score 1008.6; DB 3; Length 1750; %; Pred. No. 1e-222; 0; Mismatches 4; Indels 1; Gaps 1; 11:11:11:11:11:11:11:11:11:11:11:11:11:

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ACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGACAAGTTACA 1028
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OPERATING SYSTEM
SOFTWARE: WOLDPE
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APPLICANT: Alnemit, Emad S.
APPLICANT: Fernandez-Alnemit, Teresa
APPLICANT: Fernandez-Alnemit, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APPDTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: OF MAKING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE Mashburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
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0; Mismatches
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                                                                                                                                                                                    SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:
                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-
TELEPANTON INFORMATION:
TELEPANTON INFORMATION:
TELEPANTON FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                COMPOTER REDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDPEFECT
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Matches 1022; Conservative
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; LOCATION: 413..1750
US-09-109-273-1
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Same
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APPLICANT: Alnemri, Enad S.
TITLE OF INVENTION: Campositions For And Methods Of Waking The Same
TITLE OF INVENTION: Campositions For And Methods Of Making The Same
FILE REFERENCE: TJU2445
CURRENT APPLICATION NUMBER: US/09/723,450
CURRENT FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PLEATION NUMBER: 08/859,167
PRIOR FILING DATE: 1997-05-20
SOFTWARE: DATE: 100 1.7
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CTHER INFORMATION: No. 6576751el Sequence
NAME/KEY: CDS
LOCATION: (413)..(1750)
US-09-723-450-1
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Patent No. 6576751
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Matches 1022; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
                         FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                     NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
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Matches 1022; Conservative
                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 413..1750
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ADDRESSEE:
                                    COUNTRY:
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         GGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGG
                   181 GGTTCTTTGCTCCATCTTGGGTGCGCCTTCCCGGCGTCTAGGGGAGCGAAGGTGAGG
                                                 TGGCAGCGGCAGGAGAGTCCGGCCGCGACAGGACGAACTCCCCCACTGGAAAGGATTCTG
                                                              GGCCCGGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08545196B
Patent No. 6080577
GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN)
FILE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1089 TGATAAC 1095
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US-08-545-196B-10
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COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MELKI, JUDITH
APPLICANT: MINNICH ARNOLD
APPLICANT: MUNICH ARNOLD
TITLE OF INVENTION: FOR SPINAL MOSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLF
STREET: PO BOX 747
CITY: FALLS CHURCH
STEWART, KOLASCH AND BIRCH, LLP
                                                                                                                                                                     COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FTILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
NAME: FARACI, C. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.8%; Score 79.4; DB 3; Best Local Similarity 73.7%; Pred. No. 3.9e-09; Matches 101; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08545196B
Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10:
SEGUIENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1357 AAAAAAAAAAAAAA 1373
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                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
E: BIRCH, E
PO BOX 747
                      STREET: FO COURCH
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                                                                                          USA
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MOLECULE TYPE:
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1262 ATCTTTTGTTACTACTAATAATGCTATAAAATAAATATCCTTGTACTTCTTAAAAAAA 1321
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Pred. No. 9e-09;
0; Mismatches 21; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
ITILE OF INVENTION: Malze Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                            by experiment
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Patent No. 6313375
                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%;
Best Local Similarity 81.2%;
Matches 91; Conservative 0
                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SUDUCE:
ORGANISM: human
IMMEDIATE SOURCE:
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                         TELEX: 236262
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 3527 base pairs
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Best Local Similarity 73.9
Matches 99; Conservative
                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 140 to 1084
; IDENTIFICATION METHOD:
US-08-909-965C-7
       212-758-2982
                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (224)...(1112)
US-09-372-422A-19
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LENGTH: 1454
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Pred. No. 3.9e-09;
0; Mismatches 36; Indels 0
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277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kuga Tetsro
APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Zhao Nanding
APPLICANT: Hashida HideljiiA
TITLE OF INVENTION: NOVEL DAN, NOVEL POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFRX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: NUCLEIC acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/909,965C FILING DATE: August 12, 1997 CLASSIPICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 322745/95 APPLICATION NUMBER: PCT/JP96/03630 FILING DATE: 12-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08909965C Patent No. 5936078 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1535 AAAAAAAAAAAAAA 1551
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NAME: LAWTENCE S. PETTY
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                                                         Query Match 5.8%;
Best Local Similarity 73.7%;
Matches 101; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRI
                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: CDNA
US-08-545-196B-12
                                                                                                                                                                                                                                                     linear
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77.8; DB 4; Length 1342;
Pred. No. 8.6e-09;
0; Mismatches 62; Indels 0
                                                                                                                        APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Datier RP
APPLICANT: Jepson, Ian
TITLE OF INVENTION: Promoters
FILE REFERENCE: PD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
BARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                           FILE REFERENCE: PUOJAPIA

CURRENT PEDLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: PCT/US99/17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER PEDLICATION NUMBER: 60/095,466

EARLIER PEDLICATION NUMBER: 60/095,466

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER PILING DATE: 1998-08-05

EARLIER PILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-06

EARLIER FILING DATE: 1998-08-06

EARLIER FILING DATE: 1998-08-06

SEARLIER PILING DATE: 1998-08-06

SEQ. ID NOS: 376

SEQ. ID NOS: 376
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                                                   Sequence 89, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.68;
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Best Local Similarity 65.0
Matches 115; Conservative
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CORGANISM: Brassica napus
US-08-821-994-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-09-489-847-89
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US-08-821-994-63
                  RESULT 11
US-09-489-847-89
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1181 AATGATTAAATCGTTTCATTTTCTAAATGTGTTATAATGTGTTTAGCCCTTTCTTGTTGC 1240
                                                                                                                                                 1250 ATTGATTCACCATAGGGATTTAATCTGTATAAATCTCTATGTTGGTCAATATCATTTCAT 1309
                                                                                                                                                                                                                            Gaps
    Indels
    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P200221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVEATOR:

FILE REFERENCE: PZ002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-03-08

EARLIER FILING DATE: 1998-03-08

EARLIER FILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-05-23

EARLIER FIL
        0; Mismatches
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R RAPPLICATION NUMBER: 60/047, 592

R APPLICATION NUMBER: 60/047, 581

R APPLICATION NUMBER: 60/047, 581

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 584

R FILING DATE: 1997-05-23
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APPLICATION UNBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/047,587
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1361 AAAAAAAAAA 1372
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EARLIER APPLICATION NUMBER: 60/047, 492
EARLIER PILITAG DATE: 1997-05-23
EARLIER PLILAGATON NUMBER: 60/047, 598
EARLIER PLILAGATON NUMBER: 60/047, 592
EARLIER APPLICATION NUMBER: 60/047, 595
EARLIER APPLICATION NUMBER: 60/047, 612
EARLIER PLILAGATON NUMBER: 60/047, 612
EARLIER PLILAGATON NUMBER: 60/047, 612
EARLIER PLILAGATON NUMBER: 60/047, 613
EARLIER APPLICATION NUMBER: 60/043, 569
EARLIER APPLICATION NUMBER: 60/043, 313
EARLIER APPLICATION NUMBER: 60/043, 313
EARLIER APPLICATION NUMBER: 60/043, 314
EARLIER PLILICATION NUMBER: 60/043, 315
EARLIER PLILICATION NUMBER: 60/056, 893
EARLIER PLILAGATON NUMBER: 60

R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R APPLICATION NUMBER: 60/056,864
R APPLICATION NUMBER: 60/056,81
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,892
R RILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
R PELLOR DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R PRILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,585
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,586
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,590
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047, 614

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,578

R APPLICATION NUMBER: 60/043,578

R APPLICATION NUMBER: 60/043,576

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,670

R APPLICATION NUMBER: 60/043,670

R APPLICATION NUMBER: 60/043,670

R APPLICATION NUMBER: 60/043,670

R APPLICATION NUMBER: 60/056,664

R APPLICATION NUMBER: 60/056,664

R APPLICATION NUMBER: 60/056,664

R APPLICATION NUMBER: 60/056,664

R APPLICATION NUMBER: 60/056,910

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,910

R APPLICATION NUMBER: 60/056,910 R APPLICATION NUMBER: 60/056,862 R FILING DATE: 1997-08-22 A APPLICATION NUMBER: 60/056,887 R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,908 R PILING DATE: 1997-08-22 R PILING DATE: 1997-08-22 R FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,669 FILING DATE: 1997-09-05 60/056,636 60/049,610 FILING DATE: 1997-06-13 1997-08-22 APPLICATION NUMBER: EARLIER EARLIER

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LENGTH: 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2179 TTATTICTATGTACAACTGATGCTTGTTCTTATTTTAATAAATTTATCAGAGTGAAAAAA 2238
                                                                                                                                                                                                                                                                                                                                              1116 ATCTGAAAATTCTTGGAAATTGTTCCATGTGATTAACATGGAACTGCCTCTACTTAATCA 1175
                                                                                                                                                                2059 ACCAGCATATITATIGAAAACAIGAGACAGGAITATAGIGCCTIAACCGAIATATITIGI 2118
                                                                                                                                                                                                    1176 TICTGAATGATTAAATCGTTTCATTTTCTAAATGTGTTATAATGTGTTTAGCCCTTTCTT 1235
                                                                                                                                                                                                                                     2119 GACTTAAAAATACATTTAAAACTGCTCTTCTGCTCTAGTACCATGCTTAGTGCAAATGA 2178
                                                                                                                                                                                                                                                                       1236 GTIGCTGTATGTTTAGATGCTTTCCAATCTTTTGTTACTACTAATAATGCTATAAAATAA 1295
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                                                           Length 2323;
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Pred. No. 2.6e-08;
1; Mismatches 54;
                                                             5.5%; Score 75.6; DB 4;
55.8%; Pred. No. 3.4e-08;
tive 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/09904615
Facture No. 6566325
GENERAL INFORMATION:
PAPLICANT: Rosen et al.
TITLE CO INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATCHILING VET: 2.00
SOFTWARE: PATCHILING VET: 2.00
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; OTHER INFORMATION: n equals a,t,g, or C
US-09-904-615-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or c
         EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                       2299 AAAAAAAAAAAAAAAA 2316
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Best Local Similarity 66.0%;
Matches 107; Conservative
                                                                                    Best Local Similarity 55.8 Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo saptens
                                                                                  Similarity
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NAME/KEY: SITE
LOCATION: (31)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-904-615-66
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                                                                   Query Match
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1231 TICTIGITGCTGTATGTTTAGATGCTTTCCAATCTTTTGTTACTACTAATAATGCTATAA 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1171 AATCATTCTGAATGATTAAATCGTTTCATTTTCTAAATGTGTTATAATGTGTTTAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1348 T--ATGITGCIGIGIACCIAAGGGITIAGTAAGGICAAGAAGGGITICAAAGTITAATAA
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Pred. No. 3.9e-08;
0; Mismatches 70; Indels
                                                                                                APPLICANT: Ruben et al. TITLE OF INVENTION: 94 Human Secreted Proteins
                                                                                                                                                                     FILE REFERENCE FOLOSTOR

CURRENT PEDLICATION NUMBER: US/09/461,325A

CURRENT FILING DATE: 1999-12-14

EARLIER APPLICATION NUMBER: PCT/US99/13418

EARLIER FILING DATE: 1999-06-15

EARLIER FILING DATE: 1998-06-16

EARLIER PEDLICATION NUMBER: 60/089,508

EARLIER APPLICATION NUMBER: 60/089,509

EARLIER PELING DATE: 1998-06-16

EARLIER PELING DATE: 1998-06-16

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EARLIER FILING DATE: 1998-06-16

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EARLIER PELING DATE: 1998-06-16

EARLIER PELING DATE: 1998-06-17

EARLIER PELING DATE: 1998-06-17

EARLIER PELING DATE: 1998-06-22

EARLIER PELING DATE: 1998-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1351 AAAAAAAAAAAAAAAAAAAA 1371
; Sequence 73, Application US/09461325A; Patent No. 6475753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.5%;
Best Local Similarity 64.2%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-325-73
                                                                                                                                                        FILE REFERENCE: PZ029P1
                                                                 GENERAL INFORMATION:
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GenCore version 5.1.6
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	OM nucleic - nu	Run on:	Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 1517243 seqs, 1124081882 residues Searched:

3034486

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Published_Applications_NA:* Database :

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SUMMARIES

Score	0 1	Query Match	Query Match Length DB ID	DB	ΩI	Description
044	4	76.1	2352	11	US-09-471-749-2	Sequence 2, Appli
325	~	74.7	2045	6	US-09-861-270-1	Sequence 1, Appli
975	89	71.1	2143	6	US-09-410-194-16	Sequence 16, Appl
360	89	62.7	2034	11	US-09-009-893-1	Sequence 1, Appli
356		62.5	1190	6	US-09-410-194-14	Sequence 14, Appl
Ξ	4	31.4	495	11	US-09-918-995-26998	Sequence 26998, A
382	4:	27.9	441	11	US-09-918-995-35401	Sequence 35401, A
37	8.8	27.2	2452	6	US-09-410-194-18	Sequence 18, Appl
354	7	25.8	490	10	US-09-833-381-436	Sequence 436, App
m	45	25.1	443	Ξ	US-09-918-995-35271	Sequence 35271, A
337	8.	24.6	2770	13	US-10-005-921-1	Sequence 1, Appl1
2	4.	23.6	1319	14	US-10-103-313-34	Sequence 34, Appl
32	324.4	23.6	1319	14	US-10-115-928-19	Sequence 19, Appl
324	4.	23.6	2597	11	US-09-009-893-5	Sequence 5, Appl1
33	4.	22.8	414	Π	US-09-009-893-23	Sequence 23, Appl
•	576	20.1	437	6	US-09-864-761-3120	Sequence 3120, Ap

SEQUENCE CHARACTERISTICS:

Seguence 27, Appl	Sequence 29, Appl	Sequence 30, Appl	Sequence 37866, A		Sequence 12673, A	Sequence 4, Appl1	Sequence 132228,	Sequence 909, App	7423	Sequence 4584, Ap		Sequence 15014, A	Sequence 11218, A	Sequence 5958, Ap			Sequence 4582, Ap	19,		320	Sequence 6263, Ap	Sequence 836, App	Sequence 107, App	Sequence 11011, A	Sequence 8414, Ap	Sequence 9419, Ap	Sequence 6625, Ap	Sequence 1692, Ap
US-09-009-893-27	us-09-009-893-29	US-09-009-893-30	US-09-918-995-37866	US-09-864-761-19899	US-09-960-352-12673	US-10-005-921-4	US-10-027-632-132228	US-10-311-455-909	US-09-918-995-7423	US-09-960-352-4584	US-09-960-352-8414	US-09-960-352-15014	US-09-960-352-11218	US-10-198-846-5958	US-09-960-352-6986	US-10-198-846-1482	US-09-960-352-4582	US-10-176-306-19	US-10-106-698-1161	US-10-205-823-320	US-09-960-352-6263	US-09-960-352-836	US-09-745-763-107	US-10-198-846-11011	US-09-960-352-8414	US-09-960-352-9419	US-10-198-846-6625	US-10-106-698-1692
11	11	11	11	6	10	13	13	12	11	10	10	10	10	14	10	14	10	15	14	14	10	10	σ	14	10	10	14	14
324	308	297	479	177	277	200	603	6535	206	416	312	375	424	882	272	465	393	2165	1092	1727	408	373	3899	5001	312	364	950	1194
17.9	15.7	15.0	13.7	12.9	9.9	6.4	6.3	5.9	5.9	υ	5.8	ۍ ه	5.8	5.8	5.8	5.7	5.7	5.7	5.7	5.7	9.6	5.6	9.6	9.6	5.6	5.6	5.6	2.6
245.4	215.4	206.4	187.8	177	90	88	86.4	81.2	80.4	80.2	79.4	79.4	79.4	79.4	79.2	78.4	78	78	77.8	77.8	77.4	77.2	77.2	77.2	76.4	76.4	76.4	76.4
17	18	19	20	c 21	c 22	23	24	c 22	. 26	c 27	c 28	c 29	c 30	c 31	c 35	c 33	c 34	32	36	37	ი 38	c 39	40	c 41	42	43	C 44	c 45

ALIGNMENTS

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Sequence 2, Application US/08471749

Publication No. US2003012411341

GENERAL INFORMATION:

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah

TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESSEE OF WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/471,749
FILIME DATE:
APPLICATION NUMBER: 09/078,402
                                                                                                                                                                                                    .....reSSEE: _....reSS:
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CETTONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0519 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO:
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                                                        Length 2352;
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                                                        DB 11;
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                                                        Score 1044.4; DB 1:
Pred. No. 1.2e-210;
0; Mismatches 11;
                                                          76.1%;
98.9%;
   LENGTH: 2352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                      Matches 1062; Conservative
                                 THP1PLB02
                      linear
                                                                Similarity
                    TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: THP1PL
CLONE: 157658
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                                        ; CLONE: 1
US-09-471-749-2
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CCCAGATCCAACTGGATTTATTAGAAAATGCCTAAAGAACATCCACAGAATAGACCTGAA
                  GACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGT
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APPLICATION NUMBER: US/09/861,270 FILING DATE: 18-May-2001 CLASSIFICATION: <UNknown>
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Pred. No. 1.2e-206;
0; Mismatches 3;
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Goeddel, David V.
TITLE OF INVENTION: Regulators of Apoptosis
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NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hilaborough
STATE: California
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Matches 1038; Conserv
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                 APPLICANT: Rimoldi, Donata
APPLICANT: Rimoldi, Donata
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
ITILE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEO ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                     Query Match 71.1%; Score 975.8; DB 9; Best Local Similarity 99.7%; Pred. No. 3.4e-196; Matches 988; Conservative 0; Mismatches 2;
       Bodmer, Jean- Luc
Steiner, Veronique
Rimoldi, Donata
Schneider, Pascal
                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (383)...(1822)
US-09-410-194-16
                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020095030A1
GENERAL INFORMATION:
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APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Irmler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
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Best Local Similarity 99.7%;
Matches 873; Conservative
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MOLECULE TYPE:
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US-09-410-194-14
                                  ; LOCATION:
US-09-009-893-1
                        NAME/KEY:
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APPLICANT: ROSEN, CRAIG A.
APPLICANT: BOSEN, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APPRESSONDERCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSIFP
                                                                                                                                                                                         AGTCTGTTCAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGA 1058
                                                                                                                                          779
                                                                                                938
                                                                                                           TTTCCTCATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGG
                                                            ACCTTGTGGTTGAGTTGGAGAAACTAAATTTGGTTGCCCCAGATCAACTGGATTTATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
                                                                                                                                                                                                                                            GICTCAAGGAICCTICAAATAACITCAGGAT 1089
                                                                                                                                                                                                                                                        960 GICTCAAGGAICCTICAAATAACTICAGGCI 990
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APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-A0(-1997
ATTONEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2034 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 2000
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                                                           333
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                                                                   ATGAAGTTGACTGCCTGCTTTCCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCC
                                                                                                                             214 CGAICGCCCAGCACCAAGICCGCTICCAGGCITICGGITTCTTIGCCICCAICTIGGGIG
                                     ı;
Length 2034;
                Indels
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Score 860.8; DB 11
Pred. No. 6.6e-172;
0; Mismatches 2;
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                1003 TGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCT
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                                                                                                                                           915 TGTTCAAGGAGCAGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT HYSEQ. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2011-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26998
LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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99.3%; Pred. No. 1.6e-81;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                    Sequence 26998, Application US/09918995; Publication No. US20030073623A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ör
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(495)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Best Local Similarity
Matches 443; Conserv
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                                                                     APPLICANT: ITMLET, MATTEN
APPLICANT: Hahne, Michael
APPLICANT: Schroter: Michael
APPLICANT: Schroter: Michael
APPLICANT: Schroter: Michael
APPLICANT: Schneider, Pascal
APPLICANT: Steiner, Veronique
APPLICANT: Himoldi, Donata
APPLICANT: Himoldi, Donata
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REPERENCE: 11141-002001
CURRENT FILING DATE: 1999-09-30
FRIOR PILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.8e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 858.2; 99.5%; Pred. No. 1.8
Sequence 14, Application US/09410194
Patent No. US20020095030A1
                                                  Thome, Margot
Burns, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.5
Matches 871; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (394)...(1056)
US-09-410-194-14
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    LENGTH: 1190
                                                              APPLICANT:
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Schneider, Pascal
Bodmer, Jean- Luc
Steiner, Veronique
Rimoldi, Donata
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Best Local Similarity 68.8%;
Matches 532; Conservative
                                                                                                                 Schroter, Michael
                                                     Tschopp, Jurg
Thome, Margot
Burns, Kimberly
                                                                                         Irmler, Marten
                                                                                                   Hahne, Michael
                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (172)...(1614)
US-09-410-194-18
                                                                                                                                                                           Hofmann, Kay
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                      APPLICANT: Tschopp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724
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                                                                                  290 TIT-CIGIIGACIGGCCCGGAGCIGIACTGCAAGACCCTIGIGAGCIICCCIAGICIAAG 348
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Pred. No. 3.5e-71;
0; Mismatches 6; Indels 1;
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                                                                                                                                                                                                Sequence 35401. Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 38054
SOFTWARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 35401
                                                                                                                    596 GACCITCIGGAIAITITACGGGAAAG 621
                                                                                                                                 469 GACCTTCTTGATATTTTACGGGAAAG 494
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COTHER INFORMATION: n = A,T,C or G
US-09-918-995-35401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 27.9%;
al Similarity 98.3%;
397; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                          US-09-918-995-35401
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Best Local 3
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189 GTCTGCCGAGGTCATTCACCAGGTGGAAGAGTGTCTTGATGAAGACGAGAAGAGGAGATGAT 248
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Pred. No. 5.5e-69;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                            APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANX 197 13 393.
PRIOR PILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTESO for Windows Version 4.0
Sequence 18, Application US/09410194 Patent No. US20020095030A1 GENERAL INFORMATION:
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Mon, Aug

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1073 TCAAATAACTTCAGGATGATAACACCCTATGCCCATTGTCCTGAACTTCTTGGA 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 443;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT RELIGHTON NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PELING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: Feastseq for Windows Version 3.0
SEQ ID NO 35271
LENGTH: 443
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                                                                                                                                                                                                                    Sequence 35271, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                           1133 AATTGTTCCA 1142
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US-10-005-921-1
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                                                                                                                                                                   Sequence 436, Application US/09833381
Sequence 436, Application US/09833381
Sequence 436, Application US/09833381
Seneral INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 436
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                                              CCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo saptens
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US-09-833-381-436/c
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                                                                                                                                                                                                                                                      9; Gaps
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24.6%; Score 337.8; DB 13; Length 2770;
Best Local Similarity 73.1%; Pred. No. 2.4e-61;
Matches 451; Conservative 0; Mismatches 157; Indels 9;
                                APPLICANT: ALTER, MICHER W.
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING CASH GENE
TITLE OF INVENTION: DISRUPTIONS
TITLE OF INVENTION: DISRUPTIONS
TITLE OF INVENTION: UNBERT WAS US/10/005,921
CURRENT APPLICATION NUMBER: US 60/254,902
PRIOR PILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASTERQ for Windows Version 4.0
SED ID NO 170
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Publication No. US20020174450A1 GENERAL INFORMATION:
                       APPLICANT: Allen, Keith D.
                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-10-005-921-1
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US-10-103-313-34
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1319;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ07C1
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
23.6%; Score 324.4; DB 14; Length
Best Local Similarity 97.6%; Pred. No. 1.1e-58;
Matches 328; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/10115928
Sequence 19, Application US/10115928
Sublication No. US20030092615A1
GENERAL INFORMATION:
PAPLICAME: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibod FILE REFERENCE: PT204C1
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 1319
                                                  CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1136)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: n equals a,t,g, or US-10-103-313-34
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1136)
                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-10-115-928-19
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Sequence 34, Application US/10103313 publication No. US20030082758A1 GENERAL INFORMATION:

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821 355 881 415 941

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APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: BIXIT, VISHVA M.
APPLICANT: GENZ, REINER L.
APPLICANT: GENZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: 32
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN 6 FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942 AATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGT 1001
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                                                                                                                                                                                                                                                                                                        762 GAGTGCTGATGGCAGAGTTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTT
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ZIP: 20005

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FTIING DATE: HEREWITH
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1;
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Pred. No. 1.6e.
0; Mismatches
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APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTOMNES STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09009893 Publication No. US20030087339A1 GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 325; Conservative (
                                                                            CDS
304..1347
                    MOLECULE TYPE: CDNA
linear
                                                                         ; NAME/KEY:
; LOCATION:
US-09-009-893-5
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TOPOLOGY:
                                                 FEATURE:
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Publication No. US2003008733941
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: GENTZ, RISHAR M.
APPLICANT: KENNY, JOSEPH J.
APPLICANT: KENNY, JOSEPH J.
APPLICANT: KENNY, JOSEPH J.
APPLICANT: KENNY, HERRE J.
APPLICANT: KENNY, HERRE J.
APPLICANT: KENNY, JOSEPH J.
APPLICAN
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                                           14 GCACGAGGCAGTGCTGATGGCAGAGATTGGTTTGGATAAATCTGATGTGTCCTC 73
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STATE: MASHINGTON
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PROR APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATPONEY/AGENT INFORMATION:
AND STREET OF AUG-1997
ATPONEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,688
REFERCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2597 base pairs
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Pred. No. 1.3e-56;
0; Mismatches 20; Indels 7;
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REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-009-893-23
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Best Local Similarity .93.1%;
Matches 367; Conservative (
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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05-09-182-155-1

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Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                       Run on:
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US-09-382-155-17

Sequence 17, Application US/09382155B

Sequence 17, Application US/09382155B

Sequence 17, Application US/09382155B

Sequence 17, Application US/09382155B

GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M

APPLICANT: CHAUDHARY, PREET M

TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS

TITLE OF INVENTION: PROTEINS CAPABLE OF USING THE SAME

FILLE REPERBORE: LAUGHARY

CURRENT APPLICATION NUMBER: US/09/382,155B

CURRENT FILING DATE: 1999-08-24

EARLIER FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN Ver. 2.1
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                               PCT - US96 10521 - 7

US-08-981 - 502 - 25

US-09-516 - 747 - 25

US-08-981 - 502 - 18

US-08-16 - 747 - 18

PCT - US96 - 10521 - 18

US-09-382 - 155 - 28

US-09-074 - 044A - 27

US-09-074 - 044A - 18

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US-09-382 - 155 - 18

US-09-382 - 155 - 26

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US-09-074-044A-17
; Sequence 17, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
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US-09-382-155-17
                                                                       8001284888888444444
800128489888844444
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COMPUTER: TOTAL COMPUTER: COMPUTER: COMPUTER: COMPUTER: SOFTWARE: WordPerfect CURRENT APPLICATION DATA: CLASSIFICATION NUMBER: US/08/859,167 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: DELUCA, MARK REGISTRATION NUMBER: TJU-REFERENCE/DOCKET NUMBER: TJU-TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 445 anino acids

TYPE: AMENICATION OF SEQ ID NO: 2: LENGTH: 445 anino acids

TYPE: AMENICATION OF SEQ ID NO: 2: LENGTH: 445 anino acids
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Patent No. 6063760
                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBL OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.1%;
Best Local Similarity 94.5%;
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philadelphia
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                                                                                                        COMPUTER:
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  STATE: Pi
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: GENG THE SAME, AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES: ADDRESSES: HOVEY, WILLIAMS, TIMMONS & COLLINS STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY STATE: MISSOURI
COUNTRY: USA
ZIP: 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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1larity 100.0%; Pred. No. 8.7e-105;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,044A
                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-859-167-2; Sequence 2, Application US/08859167; Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: not relevant MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-074-044A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816/474-9057
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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Best Local Similarity
Matches 221; Conservat
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                                                                                                                                                                                                                                121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Allemri, Emad S.
APPLICANT: Allemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
WUMBER OF SEQUENCES: 17
                                                                                          1 MSAEVIHQVEEALDIDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                        NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
                                                     Gaps
                                                  ö
Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1015; DB 3;
Pred. No. 2.3e-94;
1; Mismatches 11;
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REGISTRATION NUMBER:
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LENGTH: 445
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APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: TEAD)-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE AND RESS.
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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                                                                                                                                                                                                                                                                                                                                        Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.1%; Score 1015; DB 3; 94.5%; Pred. No. 2.3e-94;
                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/859,167
                                                                                                NAME: DeLuca, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09276993; Sequence 10, Application US/09276993; Patent No. 6207801; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  LENGTH: 445 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.55
Matches 207; Conservative
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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APPLICATE ALIGNATION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, TITLE OF INVENTION: Compositions For And Methods Of Making The Same.

TITLE OF INVENTION: Compositions For And Methods Of Making The Same.

FILE REFERENCE: TJU2445

CURRENT APPLICATION NUMBER: US/09/723,450

PRIOR APPLICATION UNDERER: 09/276,993

PRIOR PILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26
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MSAEVIHQVEEALDIDEKEMILFICRDVAIDVVPPNVRDLIDILKERGKLSVGDLAELLY
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Pred. No. 2.3e-94;
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; OTHER INFORMATION: No. 6576751el Sequence
US-09-723-450-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09723450 Patent No. 6576751 GENERAL INFORMATION:
               REFERENCE/DOCKET NUMBER: TJU-
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
33,229
                                                                                                                                                                                                                                                                                                                               91.1%;
94.5%;
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 94.55
Matches 207; Conservative
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; ORGANISM: Homo sapiens
US-09-069-023-34
                GENERAL INFORMATION:
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                                                                    181 SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNC 219
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94010

ZIP: 94010

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,088A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
90.4%; Score 1007; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 202; Conservative 1; Mismatches 0;
                                                                                                                                                                   Sequence 2, Application US/08795088A
Fatent No. 6242569
GENERAL INFORMATION:
APPLICANT: Sul, Hong-Bing
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: Regulators of Apoptosis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE S.
ADDRESSEE: Science & Technology Law Group
STRREET: 75 Denise Drive
CITY: Hillsborough
STATE: California
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SYRNVLQAAIQKSLKDPSNNFRM 203
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ATTORNEY/AGENT INFORMATION:
NAME: OSMBAT, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-795-0888-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-069-023-34
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; Sequence 34, Application US/09069023A

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61 RYRRFDLLKRILKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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Sequence 2, Application US/0907404A

Patent No. 6207458

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APPOPROSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400

GITY RANSAS CITY
STATE: MISSORII

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Loseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                           Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 987; DB 4; Length 48
Pred. No. 1.7e-91;
1; Mismatches 3; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%;
98.0%;
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NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.0°
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
EBNGTH: 84
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APPLICANT: HOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
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Pred. No. 1.5e-33;
0; Mismatches 2; Indels
                                                                                                                                                                                                     Length 84;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                               Query Match 37.4%; Score 417; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 84; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMEER: US/09/382,1558
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMEER: 09/074,044
EARLIER FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                              150 DLLEKCLKNIHRIDLKTKIQKYKQ 173
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US-09-382-155-2
: Sequence 2, Application US/09382155B
: Patent No. 6160095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09382155B Patent No. 6160095 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HUMAN HERPESVIRUS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 36.2%;
1 Similarity 97.6%;
82; Conservative
                                                                         not relevant
                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                     TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                   TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                             US-09-074-044A-2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-kB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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                                                                                                                                                                  Length 78;
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SOFTWARE: PATENTIN Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS STREET: 2405 GRAND BLVD., SUITE 400 CITY: KANSAS CITY
                                                                                                                                                                34.5%; Score 384; DB 3; I ilarity 100.0%; Pred. No. 1.1e-31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.5%; Score 384; DB 3; I
100.0%; Pred. No. 1.1e-31;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09074044A Patent No. 6207458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFRENCE/POCKET NUMBER: 2658
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                               61 RVRRFDLLKRILKMDRKA 78
                                                                                                                                                                                                                                                                                                                            61 RVRRFDLLKRILKMDRKA 78
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 78
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                     ; ORGANISM: Homo sapiens US-09-382-155-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 78; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                Query Match
Best Local Similarity
Matches 78; Conserv
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Sequence 2, Application US/08807200 Patent No. 5837837 GENERAL INFORMATION:
                                                                        REFERENCE/DOCKET NUMBER: 265E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEPHOR: 816/474-9050
TELEPHOR: 820 ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                      64; Conservative
                                                                                                                                                                                                                                                          TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-807-200-2
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US-09-074-014A-21

Sequence 21, Application US/09074044A

Sequence 21, Application US/09074044A

Sequence 21, Application US/09074044A

GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M

APPLICANT: CHAUDHARY, PREET M

TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

STREEF: 2405 GRAND BLVD., SUITE 400

CITY: KANSAS CITY

COUNTRY: USA

2777
                                                                                                                              Sequence 21, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: CHAUDHARY, PREET M
APPLICANT: CHAUDHARY, PREET M
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REPERENCE: Chaudhary
CURRENT FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 KISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQ----- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL-IFL--MKDYMGRG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.6%; Score 218.5; DB 3;
Best Local Similarity 29.9%; Pred. No. 2.8e-14;
Matches 64; Conservative 41; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Molluscum contagiosum virus US-09-382-155-21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                             RVRRFDLLKRILKMDRKA 78
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1
                                                                                                                      US-09-382-155-21
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LENGTH: 241
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67 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL-IFL--MKDYMGRG 123
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                                                                                                                                                                             Gaps
                                                               Length 241;
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APPLICANT: Shighan, Andraw W.
APPLICANT: Shighan, Andraw W.
APPLICANT: Wong, Grace H.W.
TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                177 ------GAGTSYRNVLQAAIQKSLKDP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 AASPSLPVRTLRRGHGASEHEQLCMPVQESSDSP 222
                                                             19.6%; Score 218.5; DB 3 29.9%; Pred. No. 2.8e-14; Live 41; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OSTGATARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,200
ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 Franklin Street CITY: Boston SPATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/807,200
27-FEB-1997
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57 -ELLYRVRREDLLKRILKMORKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                              6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI----LRERGKLSVGDLA-- 56
                                                                                                                                                                                                                                                                                                                                Query Match
17.5%; Score 195; DB 2; Length 220;
Best Local Similarity 27.6%; Pred. No. 5.9e-12;
Matches 54; Conservative 54; Mismatches 70; Indels 18; Gaps
  35,283
BER: 07334/021001
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334
TELECOMMUICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-6906
TELEFAX: 617-542-8906
TELERAX: 200154
INFORMATION FOR ESO ID NO: 2:
SEQUENCE CHARACTER.FICS:
LENGTH: 220 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Alinear
MOLECULE TYPE: protein
US-08-807-200-2
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August 13, 2003, 16:21:28; Search time 38.1469 Seconds (without alignments) 919.565 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                              Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database :

1107863

Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

| SIDSI/gcgdata/geneseq/geneseqp-embl/Aa1980.DAT:*
| SIDSI/gcgdata/geneseqy-embl/Aa1981.DAT:*
| SIDSI/gcgdata/geneseqy-embl/Aa1981.DAT:*
| SIDSI/gcgdata/geneseqy-embl/Aa1982.DAT:*
| SIDSI/gcgdata/geneseqy-embl/Aa1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMARIES	Query re Match Length DB ID Description	100.0 221 19 AAW76630	100.0 221 19 AAW78904	100.0 221 20 AAY57455	100.0 221 20 AAY05789	100.0 221 21 AAB03959	100.0 221 22 AAB84802	100.0 221 22 AAB61117	100.0 221 23	370 23 AAR26110
di	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	1114	1114	1114	1114	1114	1114	1114	1114	4
	Result No.	, ,	ţ	e	4	ស	Q	7	80	þ

Human FLAME-1 prot Human FLAME-1 prot	ı ک	Usurpin-beta polyp	Human CFLIP-L prot	Human G1 protein 1	Human Casper prote	I-FLICE-1 protein.	Human FIN-1. Homo	Human FLICE-like i	Human MACH related	FLICE-like inhibit	. Usurpin-alpha poly	Human apoptosis as	Human FLIP-c prote	FLIP with detectab	Human CLARP protei	Usurpin-gamma poly	Human FLIP protein	Mouse CFLIP-L prot	FLICE-like inhibit	Mouse FLIP-c prote	Mouse FLIP-c prote	Mouse FLIP-c prote	Amino acid sequenc	Murine FLIP protei	Human gene 9 encod	Novel human neopla	Human apoptosis re	Human MACH related	MRIT alpha 3 polyp	I-FLICE-2 protein.	Human FLIP protein	Human liver peptid	Peptide #3127 enco	Peptide #3149 enco
AAE26086	AAY05795	AAY67419	AAW76631	AAW78903	AAW69715	AAW69229	AAW58578	AAY57454	AAY05787	AAB03960	AAY67418	AAY57606	ABB09294	AAB03964	AAY59414	AAY 67420	AAW76625	AAW76632	AAB03958	ABB09295	ABB09296	ABB09292	ABB99383	AAW76626	AAE09601	AAU21591	ABG78973	AAY0578B	AAY05791	AAW69230	AAW76215	ABG50496	ABB30476	ABB35643
20	20	21	19	19	19	19	19	20	20	21	71	21	23	21	21	21	19	19	21	23	23	23	24	19	22	22	23	20	20	19	19	22	22	22
445	227	462	480	480	480	480	480	480	480	480	480	480	480	491	480	291	479	481	481	481	218	484	484	483	391	391	391	366	384	348	104	93		66
91.1	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	4.06	4.06	90.4	90.4	90.4	88.6	•	٠.	•		64.0	m.	ω,	ω.	62.2	7	7	7	47.5	7	٠		41.7	41.7	41.7
1015	1001	1001	1007	1007	1007	1007	1007	1007	1007	1007	1007	1007	1007	1001	987	985.5	984.5	713	713	713	701.5	701.5	701.5	693	532	532	532	529	529	527	499	465	465	465
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

									treatment;	
									Death effector domain; human; murine; anti-apoptotic; treatment;	HIV infection; autoimmune disease; FLIP protein.
	21 AA.								murine;	ease; FLI
	AAW76630 standard; Protein; 221 AA				12-JUL-1999 (first entry)	1	ein.		in; human;	oimmune dis
	dard;				(firs		prote		r dom	; aut
	30 stan		30;		-1999		Human CFLIP-S protein.		effecto	fection
LT 1 6630	AAW766		AAW76630;		12-JUL		Human		Death	HIV in
RESULT 1	a	×	AC	×	DŢ	×	DE	×	ΚW	ΚW

ALIGNMENTS

97DE-1013393. DE19713393-A1. Homo sapiens. 01-APR-1997; 08-OCT-1998.

Bodmer J, Burns K, French EL, Hahne M, Hoffmann K; Irmler M, Rimoldi D, Schneider P, Schroeter M, Steiner V; Thome M, Tschopp J, Hofmann K; 97DE-1013393 (TSCH/) TSCHOPP J. (APOT-) APOTECH SA. 01-APR-1997;

WPI; 1998-532710/46. N-PSDB; AAV61936.

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                                                                                                                                                                                                                                                                           RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                                                                                                                               9
                                                       This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and autoimmune diseases.
                                                                                                                                                                                      1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                         Gaps
  New DNA encoding for anti-apoptotic gene product - used to treat HIV infections and autoimmune diseases
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G1 protein; CASH-beta; human; caspase homologue; Fas receptor;
modulator; apoptosis; cell death; inflammation; tumour; HIV;
                                                                                                                                   DB 19; Length 221;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brodlanski V, Goltsev Y, Kovalenko A, Varfolomeev E;
                                                                                                                                                                                                                                                                                                                       SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNCSM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93..142
/note= "death domain/MORT module"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "death domain/MORT module"
                                                                                                                                   100.0%; Score 1114; DB 19;
100.0%; Pred. No. 2.4e-95;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G1 protein isoform beta (CASH-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       AAW78904 standard; Protein; 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LID.
                                        Claim 20; Fig 4A; 45pp; German.
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97IL-0120367.
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                                                                                                                                                 Best Local Similarity 100.
Matches 221; Conservative
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                                                                                                                   221 AA;
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03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                              AAW78904;
                                                                                                                   Seguence
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                                                                                                                                        Query Match
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This is the amino acid sequence of the beta isoform of novel thuman G1 protein. The sequence is deduced from an isolated skin thuman G1 protein. The sequence is deduced from an isolated skin thousant cDNA clone (see AAV52895). G1-beta (also called CASH beta, G2SH being caspase homologue) and a longer isoform, G1-alpha (see CASH being caspase homologue) and a longer isoform, G1-alpha (see CASH being caspase homologue) and a longer isoform. These G1 proteins are capable of binding to the first modules, with MORT-1 or with MORT-1 binding proteins such as McH4 (CASP-10) and MACH (CASP-8), and indirectly, via their N-terminal MORT modules, with MORT-1 or with CC charles and proteins such as McH4 (CASP-10) and MACH (CASP-8), and the p55 tumour necrosis factor (INF) receptor, to which MORT-1 binds, or of binding to the intracellular domain of the p55 tumour necrosis factor (INF) receptor, to which mort-1 binds, or of binding to the intracellular considered as mediators or modulators of FAS-R having a role in the signalling process or initiated by the binding of FNE to p55-R. The longer isoform also cinitiated by the binding of FNE to p55-R. The longer isoform also considered as appease activity region involved in cytocoxic activity. G1 DNA (I) and polypeptide (II), vectors and fragments or used to requlate cell death, or inflammatory processes. (I) and (II) regulate the FAS-R ligand or TNF effect on cells carrying an FAS-R or p55-R. Tumour, HIV-infected or other considered cells can be treated using a viral vector encoding a viral curface protein, which binds a specific cell aviface receptor and a sequence encoding (II), which kills the cell. Antisense considering an also be regulated the above effects. These conservances in a cellular mRNA encoding (II), and allows (II) and can also regulate the above cector blocking and allows (II) and can also regulate the above effects.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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    New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate the effects of FAS and tumour necrosis factor receptors, useful for killing of cells e.g. HIV and cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, FLICE-like inhibitory protein long form; FLIP-L; FLIP-S; FLICE-like inhibitory protein short form; apoptosis inhibitor; arteriosclerosis; vascular wall inflammation; vascular injury;
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protein which bind MORT-1 - and
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100.0%; Pred. No. 2.4e-95;
Live 0; Mismatches 0;
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                                                                                            Claim 13; Fig 2; 132pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 221; Conservative
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98WO-US21132 97US-0946226

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Identifying regulators of MACH-related inducer of toxicity
                                                                             (UNIW ) UNIV WASHINGTON
                                                                                                                        WPI; 1999-277275/23.
N-PSDB; AAX25510.
                                                       07-OCT-1997;
                                                                                                   Chaudhary PM;
                                  07-0CT-1998;
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                                                                                                                                                                                                                                                      The present sequence represents human FLICE-like inhibitory protein short form, designated FLIP-S. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FLIP molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRIT beta 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; aplastic anaemia; myocardial infarction; therapy.
                                                                                                                                                                                                            Treating conditions characterized by vascular wall inflammation
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                     Length 221;
 Fas ligand-mediated apoptosis; atherosclerosis; transplant.
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MACH related inducer of toxicity MRIT beta 1.
                                                                                                                                                                                                                                                                                                                                                                   tch 100.0%; Score 1114; DB 20; sal Similarity 100.0%; Pred. No. 2.4e-95; 221; Conservative 0; Mismatches 0;
                                                                                                                                  (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
                                                                                                                                                                                                                                  Example 2; Page 72; 105pp; English.
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                                                                                      99WO-US03558
                                                                                                           980S-0075471
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                              221 AA;
                                                                                                                                                                                       N-PSDB; AA239041
                                                                                                                                                                                                                                                                                                                          vascular injury.
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                       Homo sapiens
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                                                                                      19-FEB-1999;
                                                                                                            20-FEB-1998;
                                          W09942570-A1
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                                                                26-AUG-1999
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                The present sequence represents novel human MACH-related inducer of toxicity (MRIT) isoform MRIT beta 1, a CED-4 homologue. Multiple isoforms of MRIT have been identified, some of which function to induce caspase dependent apoptosis in mammalian cells, e.g. mrit alpha 1 (see AAY05787) and MRIT beta 1, while others have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT beta 1 lacks the N-terminal death effector domain of MRIT alpha 1 but includes a C-terminal caspase ICE homology domain region. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation. A cell accumulation disorder such as cancer, autoimmune disease, viral infection, anglogenesis or atherosofierosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or Allos can be treated by administering an agent that selectively inhibits MRIT apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1114; DB 20; Length 221; 100.0%; Pred. No. 2.4e-95;
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Example 1; Fig 1H; 78pp; English.
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Matches 221; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AA;
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combination polypeptide which comprises a portion of an anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is described. The transport group is described. The transport group c is appain of transporting the chimeric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits has and THF mediated apoptosis by inhibiting binding of Caspase-8 to the Fas receptor complex, thus so that fusion peptide are useful for inhibiting ligand-induced apoptosis of by bringing them into contact with T cells. The chimeric group is cuseful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing T cells antigens such as tumour-specific antigen, for enhancing T cells antigens and as tumour-specific antigen, for enhancing T cells also useful for theappetist of chronically activated CD4*+ T cells in HTV infected patients. The chimeric group is also useful for theappetic, prophylactic or diagnosis of intracellular delivery of small molecules and mucleic acids encoding such polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport
FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte; tumour specific antigen; immune response; therapy; prophylaxis; diagnosis; HIV; human immunodeficiency syndrome; AIDS; acquired immune deficiency syndrome; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; score 1114; DB 21; Length 221; 100.0%; Pred. No. 2.4e-95; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNCSM 221
                                                                                                                                                                                                                                                                                                               MAYO-) MAYO FOUND MEDICAL EDUCATION & RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 78-79; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Algeciras-schminich A;
                                                                                                                                                                                                                                                                                                                                    (PAYA/) PAYA C.
(ALGE/) ALGECIRAS-SCHMINICH A.
                                                                                                                                                                                                                         05-APR-2000; 2000WO-US09002.
                                                                                                                                                                                                                                                           99US-0127867.
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Best Local Similarity 100.
Matches ,221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-664988/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AA;
                                                                                                                                                    WO200059935-A1
                                                                                               Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                           05-APR-1999;
06-APR-1999;
                                                                                                                                                                                        12-OCT-2000
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GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Testing candidate compound affecting cellular NFkappaB JNK, apoptosis activity by comparing cell activity in presence and absence of proteinaceous species having two death effector domain and test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to testing candidate compounds to determine whether they affect NF-kappab. JNK and apoptosis activity. The method involves the use of 2 death effector domains (DED). The compounds identified by the invention have therapeutic applications and are useful for regulating cellular NFkappaB. JNK and apoptosis activity. The assay is useful for identifying pharmacological agents or lead compounds generally involved in assaying for compounds which regulate or modulate a cell activity. The present sequence is a prodoamin used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NF-kappaB; JNK; apoptosis; death effector domain; DED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1114; DB 22;
100.0%; Pred. No. 2.4e-95;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 47-50; 62pp; English.
AAB84802 standard; Protein; 221
                                                                                                                                                                                                             98US-0074044
                                                                                                                                                                                                                                        98US-0074044
                                                      12-JUL-2001 (first entry)
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221; Conservative
                                                                                                                                                                                                                                                                  (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                           Chaudhary PM, Hood L;
                                                                                Huamn MRIT prodomain.
                                                                                                                                                                                                                                                                                                                    WPI; 2001-342087/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA;
                                                                                                                                                                                                               07-MAY-1998;
                                                                                                                                    Homo sapiens
                                                                                                                                                           US6207458-B1
                                                                                                                                                                                                                                      07-MAY-1998;
                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local
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AAB61117 standard; protein; 221

RESULT 7 AAB61117 AAB61117;

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WPI; 2002-401983/43.
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                                                                                                                                                                                                                N-PSDB; ABL52332
                                                                               WO200224717-A1.
                                                            Homo sapiens
                                                                                                    28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                             The present sequence has been shown to regulate the nuclear factor-kappa B (NF-kB), Jun N-terminal Kinase (JuNK) and apoptosis pathways. It is provided in a specification relating to novel mutants (D73A, L74A and L75A) for Caspase-8, which are also useful for regulating NF-kB, JuNK and apoptosis activities. The Caspase-8 mutants are useful for therapeutic purposes and in test methods or assays for determining whether a candidate compound has a significant effect upon cell activities, especially NF-kB, JuNK and apoptosis, so as to facilitate the discovery and/or design of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                             ...... mucdnts D73A, L74A and L75A for Caspase 8 useful for regulating nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities for therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSAEVIHQVEEALDīDEKEMILFICRDVAIDVVPPNVRDLIDILRERGKLSVGDLAELLY

MSAEVIHQVEEALDīDEKEMILFICRDVAIDVVPPNVRDLIDILRERGKLSVGDLAELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
                                               Human; MRITalpha; apoptotic; nuclear factor-kappa B; NF-kB;
Jun N-terminal kinase; JuNK; apoptosis; Caspase-8 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNCSM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1114; DB 22; 100.0%; Pred. No. 2.4e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                          Example 8; Column 43-46; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human FLIP-c protein SEQ ID NO:10.
                                                                                                                                                                               (UNIW ) UNIV WASHINGTON. (STOW-) STOWERS INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB09293 standard; Protein; 221
                                                                                                                                          99US-0382155
                                                                                                                                                             98US-0074044
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         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         221; Conservative
                                                                                                                                                                                                             Chaudhary PM;
                                                                                                                                                                                                                                WPI; 2001-101569/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 221 AA;
                             Human MRITalpha
         02-MAY-2001
                                                                              Homo sapiens
                                                                                                                                         24-AUG-1999;
                                                                                                                                                            07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002
                                                                                                  US6160095-A.
                                                                                                                     12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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EX DX SX B
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The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule (II) encoding a natural dominant congative regulator of caspase 8, FLIP-c, where (I) specifically hybridises with and inhibits expression of the protein, or specifically hybridises with and inhibits expression of the protein, or specifically hybridises with an least an 8-nucleobase portion of an active site on (II). (I) has antiinflammatory and anti-tumour activities. (I) is an inhibitor of FLIP-c expression, a modulator of apoptosis and can be used in antisense gene therapy. (I) is useful for inhibiting the expression of FLIP-c in cells or tissues, and for treating an animal having a disease or condition associated with FLIP-c. (I) is also useful for modulating apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is also useful for diagnostics, therapeutics, prophylaxis, as research reagents and Kits, for distinguishing functions of various members of a biological pathway, and in antisense gene therapy. (I) is also useful community for the present sequence represents human FLIP-c as given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
phosphorothloate; antisense modulation; infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense compound that hybridizes and inhibits nucleic acid encoding a natural dominant negative regulator of caspase 8, FLIP-c, useful for preventing or delaying infection, inflammation or tumor formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricketts W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 116-117; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2001; 2001WO-US28732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-2000; 2000US-0666269.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ackermann EJ, Bennett
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AAW90107 standard; Protein; 445 AA.
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA;
                                                                                                                                                                                                                                                                                                                          WO9852963-A1
                                                                                                                                                                                                                                                                                                                                                               20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1997;
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                              26-NOV-1998.
                                                          12-APR-1999
                                                                                                                                                                                                                                                                    Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                       Alnemri ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                       AAW90107;
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                       Domain
                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                Region
   RESULT 10
                                                                                                                                               Key
            AAW9010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                                                                                                                                                                                                                                                           Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting apoptosis, treating diseases characterized by apoptosis e.g. HIV infection and Alzheimer's disease, and for identifying modulators of
                                                                              Human; FADD-11ke apoptotic/anti-apoptotic protein; Alzheimer's disease; gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAEILLY
                                                                                                                                                                                                                                                                                                                                                                                                    FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME sequences are useful for inhibiting apoptosis and for gene therapy of diseases characterised by apoptosis including HIV infection and Alzaheimer's disease. FLAME inhibitors are useful as apoptotic agents and activators are useful as anti-apoptotic agents. FLAME-1 is useful as a substrate for caspase in assays to identify caspase inhibitors. The present sequence is human FLAME-1b protein.
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to FADD-like apoptotic/anti-apoptotic proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.1%; Score 1015; DB 23; Length 270; 94.5%; Pred. No. 4.7e-86; ive 1; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYRNVIQAAIQKSIKDPSNNFRSIPEERYKMKSKPLGIC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNC 219
                                                                                                                                      Location/Qualifiers
232..270
/note= "FLAME-1b unique region"
        ¥
      AAE26110 standard; Protein; 270
                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 1A; 35pp; English.
                                                                                                                                                                                                                                                                      (UXJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                 28-OCT-1997; 97US-0959167.
26-MAR-1999; 99US-0276993.
28-NOV-2000; 2000US-0723450.
                                                                                                                                                                                                                 22-AUG-2001; 2001US-0935223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 94.5
207; Conservative
                                              (first entry)
                                                                 Human FLAME-1b protein.
                                                                                                                                                                                                                                                                                                             WPI; 2002-642259/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA;
                                                                                                                                                                              US2002086983-A1.
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            the protein
                                                                                                                                                                                                04-JUL-2002.
                                              14-NOV-2002
                                                                                                                                                                                                                                                                                           Alnemri ES;
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Best Local S
Matches 207
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                                                                                             gene thera
FLAME-1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                           AAE26110;
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AAE26110
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This is the amino acid sequence of human FLAME-1, or FADD-like apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel apoptotic protein that interacts specifically with FADD, Mch4, mch5 and FLAME-2. It is recruited to the Fas receptor complex and can abrogate FasyTNF-induced apoptosis upon expression in FasyTNF-induced from the nucleotide sequence (see AAV74136) of cfFLAME-1 was deduced from the nucleotide sequence (see AAV74136) of a Jurkat cell-derived cDNA clone. Host cells, recombinant vectors, and methods of using FLAME-1 to identify substrates, activators or inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see AAW90108) and agonists can be used to inhibit apoptosis, e.g. for treating interaction or Alzheimer's disease. Inhibitors can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oŧ
                                                                                                                                                                                                                                                                                                                                                                                  /note= "pl2 subunit, specifically claimed in Claim
4"
                                                                                                                                                                                                                                                                                             /note= "p39 subunit, specifically claimed in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated FADD-like anti-apoptotic molecules - used to develop apoptotic and anti-apoptotic agents for treating, e.g. HIV infection, Alzheimer's disease or neoplastic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "active site mote...
338..342
/note= "caspase cleavage site, generating p39 and
p12"
                                                   FLAME-1; FADD-11ke apoptotic/anti-apoptotic molecule; human; apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "caspase-domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90..168
/note= "FADD-DED homology B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "FADD-DED homology A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 39-40; 68pp; English.
                                                                                                                                                                                                                                  Location/Qualifiers
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322..32
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Human FLAME-1 protein.
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N-PSDB; AAV74136.
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WPI; 1999-277275/23
                                                                  445 AA;
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                                                                  Sequence
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                                                                RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting apoptosis, treating diseases characterized by apoptosis e.g. HIV infection and Alzheimer's disease, and for identifying modulators of
                                                                                                                                                                                                                                               Human; FADD-11ke apoptotic/anti-apoptotic protein; Alzheimer's disease;
gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
FLAME-1.
                                        MSAEVIHOVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to FADD-like apoptotic/anti-apoptotic proteins
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                                                                                                                                                                                                                                                                                                                                                      "Caspase-domain homology (CDH) region"
 Length 445;
                                                                                                                                                                                                                                                                                                              /note= "FADD-DED-Homology A (FDH-A) region"
90..168
                                                                                                                                                                                                                                                                                                                                      "FADD-DED-Homology B (FDH-B) region"
                 Indels
                                                                                                                               SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNC 219
                                                                                                                                         SYRNVLQAAIQKSLKDPSNNFRSIPEERYKMKSKPLGIC 219
DB 20;
Score 1015; DB 2C
Pred. No. 8.8e-86;
1; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                             /note= "Caspase cleavage site"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                       AAE26086 standard; Protein; 445
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91.1%;
94.5%;
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2000US-0723450.
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                                                                                                                                                                                                                       (first entry)
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/note= "C
323..327
                 207; Conservative
                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                      Human FLAME-1 protein.
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N-PSDB; AAD43202.
        Similarity
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Query Match
Best Local 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
(FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME sequences are useful for inhibiting apoptosis and for gene therapy of diseases characterised by apoptosis including HIV infection and Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and activators are useful as anti-apoptotic agents. FLAME is useful as a substrate for caspase in assays to identify caspase inhibitors. The present sequence is human FLAME-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-apoptotic; cancer; autoimmune disease; angiogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection; aplastic anaemia; myocardial infarction; therapy; mutent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The results
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                           Length 445;
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                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYRNVIOAAIOKSLKDPSNNFRSIPEERYKMKSKPLGIC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNC
                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.8e-86;
1; Mismatches 11;
                                                                                                                                                                                                                                                                                                              Score 1015;
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                                                                                                                                                                                                                                                                                                    Query Match 91.1%;
Best Local Similarity 94.5%;
Matches 207; Conservative
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Claim 20; Fig 4B; 45pp; German
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                                                                                                               462 AA;
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Irmler M,
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                                                                                                                 Sequence
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immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA molecules and polypeptides for treating apoptosis e.g. autoimmune diabetes, cancer and Parkinson's
                                                                                                                                                                                                                                  GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
                                                                                                                                                      1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                                 The invention provides recombinant nucleic acid molecules encoding usurpin-alpha (lacking the first death effector domain (DED) or its prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
                                                                                                                                      Gaps
 sufficient for FLICE-P20 interaction. The invention provides multiple isoforms of MRIT (see AAY05787-89), isolated active fragments of which have either pro-apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors of MRIT apoptotic the dysfunction of programmed cell death or proliferation, such as cancer or a neurodegenerative disorder.

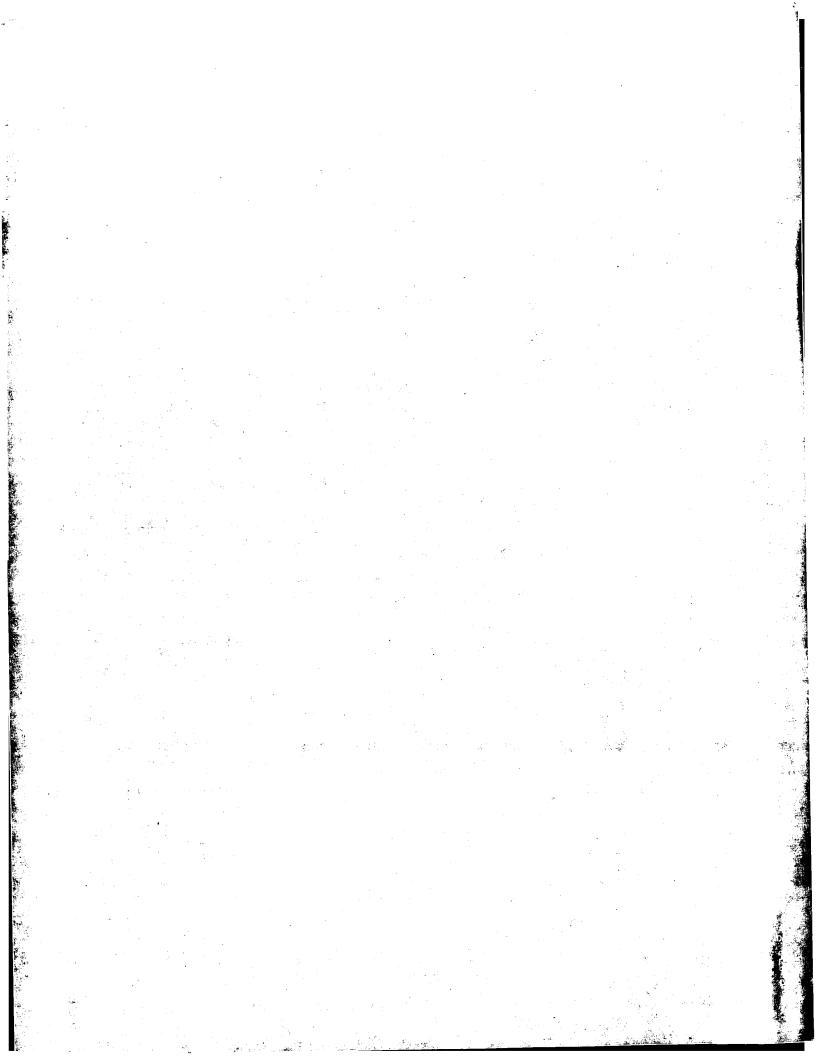
Whote: the present sequence is not shown in the specification but is derived from the MRIT alpha I sequence given in figure IF.
                                                                                                                                     ô
                                                                                                                 Length 227;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Usurpin-alpha; death effector domain; DED; prodomain; usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; caspase; cytostatic; antiParkinsonian; antidiabetic.
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                                                                                                                 Score 1007; DB 20;
Pred. No. 2.1e-85;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                              AAY67419 standard; Protein; 462
                                                                                                                    90.48;
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                                                                                                                                       Matches 202; Conservative
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mediated diseases
                                                                                                                             Similarity
                                                                                                   227 AA;
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N-PSDB; AAZ56988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for in vitro and in vivo identification of usurpin-procaspase-8 interaction inhibitor. Usurpin is useful as modulator of the sensitivity of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis is useful for treating diseases like autoimmune diabetes, cancer and parkinson's disease. Activators and inhibitors of usurpin-procaspase-8 interaction are also useful for treating various diseases mediated by apoptosis. Usurpin provides an attractive model for modulating caspase activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be regulated at several levels in the presence of usurpin, conferring resistance to Fas-ligand cell death. The present sequence represents the usurpin-beta polypeptide.
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HIV infection; autoimmune disease; FLIP protein.
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                                                                                                                                                                                                                                                                                                                                                                                             90.4%; Score 1007; DB 21; Length 462; 99.5%; Pred. No. 5.1e-85; ive 1; Mismatches 0; Indels 0
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Schneider P, Schroeter M, Steiner
Hofmann K;
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This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and
                                                                                                                                          61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM
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                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
modulator; apoptosis; cell death; inflammation; tumour; HIV;
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                                                                                 Length 480;
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93..142
/note- "death domain/MORT module"
                                                                              Score 1007; DB 19;
Pred. No. 5.4e-85;
1; Mismatches 0;
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971L-0120367.
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N-PSDB; AAV52968.
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OM protein - protein search, using sw model

August 13, 2003, 16:33:14; Search time 9.45792 Seconds (without alignments) 1098.857 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-380-546A-4 1114 1 MSAEVIHQVEEALDTDEKEM.....RMITPYAHCPDLKILGNCSM 221

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	015519 h casp8 and		mollusc	O89110 mus musculu	Q14790 h caspase-8	•		_	013158 homo sapien		Q8ya96 listeria mo	P94899 leuconostoc	Q14573 homo sapien	•	Q63269 rattus norv				P15215 drosophila			_	-	Q60737 mus musculu		_		_	Q9z9ml bacillus ha	schizosac	Q8yud4 anabaena sp	5 methanocc	P21869 gallus gall
SUMMARIES	ţ	ar	CFLA_HUMAN	CFLA_MOUSE	CFLA_MCV1	ICE8_MOUSE	ICE8_HUMAN	CFLA_HSVE2	ICEA_HUMAN	VG71_HSVSA	FADD_HUMAN	RPOC_LISIN	RPOC_LISMO	RPOC_LEUPS	IP3T_HUMAN	YCIMLECOLI	IP3T_RAT	RPOC_LEUME	RPOC_BACSU	RPOC_WEIHE	LMG1_DROME	RPOC_PEDAC	RPOC_STAAU	MTLD_CLOAB	VN34_ROTBU	KC21_MOUSE	KC22_XENLA	VAV_DROME	RPOC_LISGR	EX5B_BORBU	RPOC_BACHD	TCPZ_SCHPO	SYA_ANASP	YB56_METJA	KC22_CHICK
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P21868 gallus gall P19138 homo sapten P33674 oryctolagus P19139 rattus norv P52960 saccharomyc P77819 bacillus an Q95mm3 chlamydomon P52150 aptroplasma Q91513 fowlpox vir Q49498 arabidopsis P96178 weissella p Q9ze20 rickettsia
KC21_CHICK KC21_HUMAN KC21_RABIT KC21_RABIT PIP2_YEAST PIP2_YEAST RPOC_BACAN DY1A_CHLRE PURA_SPICI V018_FOWPV DML3_ARATH RPOC_WEIPA
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ALIGNMENTS

Paya C.V.;

Griffith T.S., Lynch D.H.,

Algeciras-Schimnich A.,

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A Straubberg R.L., Feingld E.A., Grouse L.H., Derge J.G.,
A Straubberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Both C.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tooshlyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterffield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,
B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Human and mouse Colk Sequences."
Human and mouse Colk Sequences."
                                                                                                                                                                                                                                                                                                  MEDLINE-99218584; PubMed-10200473;
Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I., Keep S.L.C., Tawa P., Kanthoudakis S., Nasir J., Martindale D., Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P., Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S., Nicholson D.W.;
                                                          Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.; "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-98021435; PubMed-9380701; Inohara N., Koseki T., Hu Y., Chen S., Nunez G.; Inohara N., Roseki T., Hu Y., Chen S., Nunez G.; CLARP, a death effector domain-containing protein interacts with caspase-8 and regulates apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
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"CASH, a novel caspase homologue with death effector domains.";
J. Biol. Chem. 272:19641-19644(1997).
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                                                                                                                                                                                               Hu S., Dixit V.M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12)
                    TISSUE-Umbilical vein endothelial cells;
MEDLINE-97362203; Pubmed-9211860;
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                                                                                                       CD-95-induced apoptosis.";
J. Biol. Chem. 272:17255-17257(1997).
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MEDLINE-22388257; PubMed-12477932;
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MEDLINE-97426025; PubMed-9289491;
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FROM N.A. (ISOFORM 1)
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for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOIG-01519-14; Sequence-VSP_000839;
TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN
SKELETAL MUSCLE, PANCREAS, HEART, KIDNEY, PLACENTA, AND PERIPHERAL
BLOOD LEUKOCYTES. ALSO DETECTED IN DIVERSE CELL LINES. ISOPORM 8
IS PREDOMINANTLY EXPRESSED IN TESTIS AND SKELFTAL MUSCLE.
INDUCTION: REPRESSED BY IL-2 AFTER TCR STIMULATION, DURING
PROGRESSION TO THE S-PHASE OF THE CELL CYCLE.
DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
                                                                                                                        ARMMALIAN CELLS. ACTS AS AN INHIBITOR OF THERSEG MEDIATED
APOPTOSIS. A PROTEDLYTIC FRACHENT (P43) IS LIKELY RETAINED IN THE
DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
RECRUTIMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
APOPTOSIS OR TO REDUCE THERSF-TRIGGERED APOPTOSIS. LACKS ENZYMATIC
(CASPASE) ACTIVITY
SUBBULIT: THERSEG STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
INDUCING SIGNALING COMPLEX (DISC) FORMED BY THRRSFG, FADD AND
CASPASE-8. A PROTEDLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
BCL-X(L) (IN VIERO).
                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms-14;
Name-1; Synonyms-FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
I, FLAME-1 gamma, Usurpin alpha;
Isoford-015519-1; Sequence-Displayed;
Name-2; Synonyms-FLIP-S, CLARP2, MRIT beta-1, CASH beta;
IsoId-015519-2; Sequence-VSP_000828, VSP_000829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVOLVED IN CATALYSIS.

PTM: PROTECUTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12. SIMILARITY: BELONGS TO PEPTIDASE FAMILY Cl4. SIMILARITY: Contains 2 death effector (DED) domains.
                    cycle-dependent regulation of FLIP levels and susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=6; Synonyms-I-FLICE 4;
IsoId=015519-6; Sequence=VSP_000826, VSP_000841;
Name=7; Synonyms-I-FLICE 5;
IsoId=015519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoid=015519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
Name=10; Synonyms=Flame-1 delta;
Isoid=015519-10; Sequence=VSP_000834, VSP_000835;
                                                                                  FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=015519-12; Sequence-VSP_000832, VSP_000833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-VSP_000834, VSP_000835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=3; Synonyms=MRIT alpha-2;
IsoId=015519-3; Sequence=VSP_000824, VSP_000838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-11; Synonyms-Usurpin beta;
IsoId-015519-11; Sequence-VSP_000838;
Name-12; Synonyms-Usurpin gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=015519-13; Sequence=VSP_000831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=4; Synonyms-I-FLICE 2;
ISOId=015519-4; Sequence-VSP_000825;
Name=5; Synonyms-I-FLICE 3;
ISOId=015519-5; Sequence-VSP_000840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=8; Synonyms=Flame-1 alpha;
IsoId=015519-8; Sequence=VSP_000830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-9; Synonyms-Flame-1 beta;
                                         Fas-mediated apoptosis.";
J. Immunol. 162:5205-5211(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF010127; AAB64110.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFLA_MOUSE STANDARD; PRT; 484 AA.

CFLA_MOUSE Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 42, Last annotation update)

16-OCT-2003 (Rel. 42, Last annotation) (Caspe precursor (Cellular FLICE-like inhibitory protein) (Caspes-eight-related protein) (Caspese-like apoptosis requiatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of FLICE) (I-FLICE) (I-F
                                                                                                                                                                                                                           1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.; "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor through c-FLIP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Irmler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D., French L.E., Tschopp J.;
"Inhibition of death receptor signals by cellular FLIP.";
Nature 388:190-195(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Immunol. 30:155-163(2000).
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J. Biol. Chem. 272:19641-19644(1997).
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         Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E., Brodianskii V.M., Wallach D.;
                                                                                           0; Indels
Score 1007; DB 1;
Pred. No. 1.3e-64;
                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYRNVLQAAIQKSLKDPSNNFRM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SYRNVLQAAIQKSLKDPSNNFRL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20350661; PubMed-10894163;
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MEDLINE-97426025; PubMed-9289491;
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90.4%;
                                                                                  Matches 202; Conservative
                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                       61
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                                         Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            ARAMALIAN CELLS. ACTS AS NI INHIBITOR OF THERSEG MEDIATED
APOPTOSIS. A PROTEDLYTIC FRACHENT (P43) IS LIKELY RETAINED IN THE
DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
APOPTOSIS OR TO REDUCE THERSF-TRIGGERED APOPTOSIS. LACKS ENZYMATIC
(CASPASE) ACTIVITY (BY SIMILARITY)
SUBUNIT: THERSEG STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
INDUCING SIGNALING COMPLEX (DISC) FORMED BY THERSF6, FADD AND
CASPASE-8. A PROTEDLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
BLISC (BY SIMILARITY).
                                                                                                                                                                                                               EVENT-ALIETRALIVE SPLICING; Named isoforms-2;
Name-1; Synonyms-FLIP-L, CASH alpha;
Isold-035732-1; Sequence-Displayed;
Name-2; Synonyms-FLIP-S, CASH beta;
Isold-035732-2; Sequence-VSP_000842, VSP_000843;
Isold-035732-2; Sequence-VSP_000842, VSP_000843;
-1-TISSUE SPECIFICITY: Highly expressed in heart.
-1-DEVELOPMENTAL STAGE: AT EMBARYONIC DAYS E9:5 AND E10.5 HIGHEST
EXPRESSION IN DEVELOPPING HEBARY.
-1-INDUCTION: ISOFORM 1 BUT NOT ISOFORM 2 IS ACTIVATED BY BCR CROSS-
LINKING IN PRIMARY B-CELLS.
-1-DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
INVOLVED IN CATALYSIS.
-1-PHY: PROCESSED; PROBABLY BY-CASPASE-8; PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT P43 (BY SIMILARITY).
CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
SUBUNIT P12 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Alternative splicing.
1 380 CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LONGRSKEPRF -> VSLEPVYGVPA (in isoform
 CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
-!- SIMILARITY: Contains 2 death effector (DED) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN REF. 2).
OBF7A92CB09F5F1F CRC64;
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Pred. No. 6.8e-43;
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Missing (in isofc
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PROSITE; PS50168; DED; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DED
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55245 MW;
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InterPro; IPR001309; ICE_p20.
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421
208
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3;
                                                                                   DYMGRGKISKEKSFLDLVVELEKLNLVAPPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQG 177
                                                                                                                                65
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"Death effector domain-containing herpesvirus and poxvirus proteins inhibit both Fas- and TWFR1-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
                                  1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                       RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL---MK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
"A random DNA sequencing, computer-based approach for the generation
of a gene map of molluscum contagiosum virus.";
Virus Genes 14:73-80(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsukumo S.I., Yonehara S.; *Requirement of cooperative functions of two repeated death effector domains in caspase-8 and in MC159 for induction and inhibition of
5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97242415; PubMed-9087414; Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E., Netpel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M., Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.; "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
                                                                                                                                                                                                                                                                                                                                                     Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of a human tumorigenic poxvirus: prediction of specific host response-evasion genes."; Science 273:813-816(1996).
                                                                                                                                                                                                                                                  CFLA.MCV1
CFLA.MCV1
CFLA.MCV1
CFLA.MCV1
CFLA.MCV1
CF.CT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral FLICE-inhibitory protein) (v-FLIR).
29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-9632459; PubMed-8670425;
Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V.,
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99457304; Pubmed-10526240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 91-241 FROM N.A. MEDLINE-97352177; PubMed-9208457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97188440; PubMed=9037025;
                                                                                                                                                                   AGTSYRNVLQAAIQK-SLK 195
                                                                                                                                                                                         A-RSNMNTLQASLPKLSIK 203
 Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death receptors.";
Nature 386:517-521(1997).
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                             Molluscipoxvirus
                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL-IFL--MKDYMGRG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 HILEE-LDSHEDSLLLFICHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71
                   Genes Celis 4:541-54971999).
-1- FUNCTION: INHIBITS THRESFIA, THERSF6 AND THERSF12 INDUCED
APOPTOSIS. MAY INTERFERE WITH CASPASE-8 RECRUITMENT AND ACTIVATION
AT THE DEATH-INDUCING SIGNALING COMPLEX (DISC). MAY LEAD TO HIGHER
VIRUS PRODUCTION AND CONTRIBUTE TO VIRUS PERSISTENCE AND
                                                                                                                                                                                                             SUBUNIT: ASSOCIATES WITH THE DEATH-INDUCING SIGNALING COMPLEX (DISC) FORMED BY THERSFE, FADD AND CASPASE-8. INTERACTS WITH FADD. SIMILARITY: Contains 2 death effector (DED) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 KISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQ----
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
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"Molecular cloning and characterization of mouse caspase-8.";
Eur. J. Biochem. 253:399-405(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 241;
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175 DED 2.
26939 MW; 155C9FB0B969E216 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.6%; Score 218.5; DB 1; Best Local Similarity 29.9%; Pred. No. 6.7e-09; Matches 64; Conservative 41; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GAGTSYRNVLQAAIQKSLKDP 197
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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CASP8.
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MEDLINE=98316661; PubMed=9654089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U60315; AAC55287.1; -.
EMBL; U86888; AAB57923.1; -.
PIR; T30761; T30761.
Interro; IPRO1875; DED.
Pfam; PF01335; DED; 2.
SMART; SM00031; DED; 2.
apoptosis, respectively.";
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Apoptosis; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kloschis P., Kischkel F., Poustka A., Krammer P.;

Kloschis P., Kischkel F., Poustka A., Krammer P.;

Kloschis P., Kischkel F., Poustka A., Krammer P.;

Submitted (JUL-1997) to the EMBL/GenBank/DbBJ databases.

-I- FUNCTION: Most upstream protease of the activation cascade of caspases responsible for the TNFRSF/FAS mediated and TNFRSFIA induced cell death. Binding to the adapter molecule FADD recruits it to either receptor. The resulting aggregate called death-laducing signaling complex (DISC) performs CASPB proteclytic activation. The active dimeric enzyme is then liberated from the DISC and free to activate downstream apoptotic proteases.

Proteclytic fragments of the N-terminal propeptide (termed CAP3) cAP5 and CAP6) are likely retained in the DISC. Cleaves and activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May participate in the GZMB apoptotic pathways. Cleaves ADPRT.

Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-I-AMC. Likely target for the cowpox virus CRMA death inhibitory protein.

-I- ENEWER ENGULATION: Inhibited by Z-VAD-FK, Crmm and P35.

-I- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit. Interacts with FADD and CFLAR (By similarity).

-I- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.

-I- Linghest expression in spleen, thymus, lung, liver and kidney.

-I- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
                                                                                                                                                                 **REDLINE=22388257; PubMed=12477932; Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer T.E., Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glusarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Schermen M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schmutz J., Myers R.M., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Generation of the subunits requires association with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           death-inducing signaling complex (DISC), whereas additional processing is likely due to the autocatalytic activity of the activated protease. GZMB and CASP10 can be involved in these
                                                      den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
                                                                                              "Molecular cloning and identification of murine caspase-8.";
J. Mol. Biol. 284:1017-1026(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processing events (By similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: Contains 2 death effector (DED) domains.
SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-99057979; PubMed-9837723;
Van de Craen M., Van Loo G., Declercq W., Schotte P.,
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                            Vandenabeele P.;
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57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNPH--LVSDYRVLMAEIGEDLDKSDVSSLI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLD-----ILRERGKLSVGDLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.7%; Score 197; DB 1; Length 480;
27.6%; Pred. No. 4.9e-07;
tive 52; Mismatches 61; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICER_HUMAN STANDARD; PRT; 479 AA. 014795; Q14796; Q14790; O14676; Q14791; Q14793; Q14796; Q15806; Q15806; Q8TDI1; Q8TDI2; Q8TDI3; Q8TDI4; Q8TDI5; Q96T22; Q9C0K4; Q9CQ81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISR -> PHPVG (IN REF. 4).

DNAQIS -> RQCPREL (IN REF. 4).

A -> V (IN REF. 2).

VMLFK -> SCSFR (IN REF. 4).

K -> N (IN REF. 4).
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045268AE3DE5ED4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASPASE-8 SUBUNIT P10.
BY SIMILARITY.
BY SIMILARITY.
DED 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASPASE-8 SUBUNIT P18.
                                                                                                                                                                                           G0; G0:0005737; C:cytoplasm; IDA.
G0; G0:0005644; C:nucleus; IDA.
G0; G0:0004205; F:caspase-8 activity; IDA.
G0; G0:0006915; P:apoptosis; IDA.
InterPro; IPR001875; DED.
InterPro; IPR002398; ICE.
InterPro; IPR002398; ICE.
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PROSITE; PSO1121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS50168; DED; 2.
                                                                                                                                                                                                                                                                                                                                Pfam; PF01335; DED; 2.
Pfam; PF00556; Peptidase_C14; 1.
PRINTS; PR00376; ILIBCENZYME.
SWART; SW00115; CASC; 1.
SWART; SW00115; DED; 2.
                               AF067839; AAC40132.1; J
AF067840; AAC40132.1; J
AF067834; AAC40131.1; -
AJ007749; AAH06737.1; -
BC006737; AAH06737.1; -
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AAC40132.1;
AAC40132.1;
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Best Local Similarity 27.6%
Matches 50; Conservative
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                                                                                                                                       Q15806; 1QDU.
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                    AF067838;
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ACT_SITE
DOMAIN
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CONFLICT
CONFLICT
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                                                                                                                                           HSSP; 01
MEROPS;
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PROPEP
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                                                                                       EMBL;
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                                                                      EMBL;
                                                                                                                          EMBL;
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                                                                                                         EMBL;
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EMBL; AF067841; AAC40132.1; -. EMBL; AF067835; AAC40132.1; JOINED.

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Muzlo M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A., Ni J., Scaffildl C., Bretz J.D., Zhang M., Gentz R., Mann M., Krammer P.H., Peter M.E., Dixit V.M.;
"FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited to the CD95 (Fas/APO-1) death-inducing signaling complex.";
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
(MORTI-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-1ike protease) (FADD-1ike ICE) (FLICE) (Apoptotic cysteine protease)
(AApoptotic protease MCh-5) (CAP4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96353838; PubMed-8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M. Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.;
Litwack G., Alnemri E.S.;
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                                                                                                                                                                                                                                         [1]

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TISSUB-B-cell, and Thymus:

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MEDLINE-99132295; PubMed-9931493;
Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
"Structure and chromosome localization of the human CASP8 gene.";
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A. (ISOFORM 2).
STINIVASULA S.M., Ahmad M., Ottille S., Bullrich F., Banks S.,
Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
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SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDLINE-96279827; PubMed-8681377;
SECOUTIVE CO. O'ROUTKE K.
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SEQUENCE FROM N.A. (ISOFORM 4).
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                                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                        NCBI_TaxID=9606;
      DDTTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDD
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A MEDLINE-22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buckwe K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K.A., Fanmer A.A., Rubin G.M., Bong L., A Stapletcon M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Soaxe S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Soaxe S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A., A Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hulting M., Madan A., Young A.C., Shevchenko Y., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ruban and mouse coll signification and initial analysis of more than 15,000 full-length benchman and mouse coll significant and signifi
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MEDLINES 97477382; PuDMed=9334338;
Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
Cromlish J.A., Shore G.C.;
"p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the endoplasmic reticulum.",
J. Cell Biol. 139:327-338(1997).
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[8] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM WITH BCAP21 AT THE ENDOPLASMIC RETICULUM.
MEDLINE-21927603; Pubmed-11917123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzio M., Salvesen G.S., Dixit V.M.; "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
Hayashi K.;
                                                                                                                                                                                                                 Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C., "The processpace-8 isoform, processpace-8L, recruited to the BAP31 complex at the endoplesmic reticulum.", Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
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Biochem. Biophys. Res. Commun. 272:877-881(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 7).
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STANDARD;

HSVE2

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57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
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7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQERRMLEESNLSFL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI----LRERGKLSVGDLA-- 56
              Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F., Wu J.C., Tomaselli K.J., Gruetter M.G.; The three-dimensional structure of caspase-8: an initiator enzyme in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       MEDLINE-22239940; PubMed-12353035, Chun H.J., Zheng L., Ahmad M., Mang J., Speirs C.K., Slegel R.M., Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S., Atkinson T.P., Straus S.E., Lenardo M.J.; Pleiotropic defects in lymphocyte activation caused by caspase-8 mutations lead to human immunodeficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                17.3%; Score 192.5; DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                      me=5; Synonyms=Beta-1;
IsoId=Q14790-5; Sequence=VSP_000814, VSP_000815;
                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q14790-4; Sequence=VSP_000809, VSP_000810;
                                                                                                                                                                                                                                                                                                                                                                                                               IsoId-Q14790-6; Sequence-VSP_000811, VSP_000812;
                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Mismatches
                                                                                                                                                                                                                                                                                                                                    Name=2; Synonyms=Alpha-2, MCH5-beta;
IsoId=014790-2; Sequence=VSP_000810;
                                                                                                                                                                                                                                                                                                                                                             IsoId-014790-3; Sequence-VSP_000813;
                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=Alpha-1;
IsoId=Q14790-1; Sequence=Displayed;
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-99451259; Pubmed-10508784;
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SVQGAGTSYRN 184
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|FSKERSSSLEGSPDEFSN 198
                                                                                                                                                                                                                                                                                                                                                      Synonyms-Alpha-3;
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                                                Structure 7:1125-1133(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                 VARIANT CASPBD TRP-248.
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                                                                                                                                                                                                                                                                                                                                                                                                        Name=6;
                                         apoptosis
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Mertin D., Armstrong R.C., Ottlie S., Martin D.A., Wang Y., Banks S.,
Mang G.H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
Tomaselli K.J., Cohen J.I.;
Tomaselli K.J., Cohen J.J., Cohen J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLLDILRERGKLSVGDLAELLYRVRRF
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                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Viral CASP8 and FaDD-11ke apoptosis regulator (v-CFLAR) (Viral PLICE-inhibitory protein) (v-FLIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95302501; PubMed-7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
"The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995).
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                                                                                                                                                                                                                                                                                                                                                      Equine herpesvirus type 2 (strain 86/87) (EHV-2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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171 AA.
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DOMAIN 1 74 DED 1.

00 171 DED 2.
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                                                                                    (Rel. 40, Created)
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SMART; SM00031; DED; 2.
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                                                                                                                     16-OCT-2001
15-SEP-2003
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Best Local
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Hadano S., Yanaqisawa Y., Skaug J., Fichter K., Nasir J.,
Hadano S., Yanaqisawa Y., Skaug J., Fichter K., Nasir J.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Ikeda J.-E., Hayden M.R.;
"Cloning and characterization of three novel genes, ALSZCR1, ALSZCR2,
and ALSZCR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
critical region at chromosome 2q33-q34: candidate genes for ALS2.";
Genomics 71:200-213(2001).
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protease Mof5 is a CTMA-linhibitable protease that activates multiple
Ced-3/ICE-like cysteine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
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SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE-97197836; Pubmed-9045686;
Vincenz C., Dixit V.M.;
"Fast-associated death domain protein interleukin-lbeta-converting enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved CD95- and p55-mediated death signaling.";
J. Biol. Chem. 272:6578-6583(1997).
                                                                                                                                                                                                                                                                ICEA_HUMAN STANDARD; PRT; 521 AA.
09281; 098708; 09945; 097207;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Apoptotic protease Mch. 4) (ReS-associated death domain protein interleukin.1B-converting enzyme 2) (FLICE2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-T-cell;
MEDLIRE-9653838; PubMed-8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.;
In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains.";
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                       122 RGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQ 169
                                                                                                                                   MEDLINE-97121412; Pubmed-8962078;
Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
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TISSUE-Spleen, and Thymus;
MEDLINE-99214592; PubMed-10187817;
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MEDLINE-99339325; PubMed-10412980;
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J. Biol. Chem. 274:10301-10308(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute of are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
Name=A; Synonyms=10-A;
IsoId=092851-1; Sequence=Displayed;
Name=B; Synonyms=10-B;
IsoId=092851-2; Sequence=VSP_000819, VSP_000820;
Name=C; Synonyms=10-C;
IsoId=092851-3; Sequence=VSP_000821, VSP_000822;
-1 TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION
IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.
-1- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
THE TWO ACTIVE SUBBNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DISEASE: Defects in CASPIO are the cause of type II autoimmune lymphoproliferative syndrome (ALPS2) [MIM:603909]. ALPS2 is characterized by abnormal lymphocyte and dendritic cell homeostasis and immune regulatory defects.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
-!- SIMILARITY: CORTAINS 2 death effector (DED) domains.
                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms-3;
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GO; GO:0004206; F:caspase-10 activity; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
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InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE.
InterPro; IPR001309; ICE_p20.
Pfam; PF01335; DED; 2.
Pfam; PF00656; Peptidase_C14; 1.
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BAB32553.1;
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AF111345; AAD28403.1;
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BAB32553.1;
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MIM; 601762; -.
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AB038975; I
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AB038979; 1
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EMBL;
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EMBL;
EMBL;
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DED 1.
DED 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50168; DED; 2.
Hypothetical protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; X64346; CAA45694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M86409; AAA46147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24....
A2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR001875, DED. SMART; SM00031; DED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN 93
SEQUENCE 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLE-----KCLKNIHRIDLKTKIQ- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSASDVFEHLLAEDLLSEEDPFFLAEL 82
                                                                                                                                                                                                                                                     Missing (in isoform B).
/FTId=VSP_000819.
MIKFLEKTWEIRGRKRTVWGAKQISATSLPTAISAQTPRPP
                                                                                                                                                                                                                                                                                                                                       /FIId-vSP_000820.
GNRAINGAPSLVSRGMQGASANTLNSETSTKRA -> EGSC
VQDESEPQRPLCHCQQPQLYLPEGQTRNP (in isoform
                                                                                                                                                                                                                                                                                                         MRRWSSVS -> HEDILSILTAVNDDVSRRVDKQGTKKQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVGD---LAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-92333688; PubMed-1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
                                                                                                                                                                                                                                                                                                                       QPAFTLRKKLVFPVPLDALSI (in 1soform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Indels
                                                                                                                                            CASPASE-10 SUBUNIT P23/17.
CASPASE-10 SUBUNIT P12.
DED 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTIG=VAR_014072.
E -> G (IN REF. 2).
T -> A (IN REF. 3).
840348AE602B8243 CRC64;
                                                                                                       Zymogen; Repeat;
        PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS50168; DED: 2.
Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat; Alternative spilcing; Polymorphism; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform C).
/FTId=VSP_000822.
L -> F (in ALPS2).
/FTId=VAR_014071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KYKQSVQG-----AGTSYRNVLQAAIQKS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_000821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical gene 71 protein.
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                                                                                                                                                                                                                     SIMILARITY. SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 160; 29.8%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 OR ECLF3.
Herpesvirus saimiri (strain 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 É
268 T
58950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                   521
97
187
358
401
271
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268
521 AA;
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                                                                                                                                                                   416
19
114
358
401
229
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Q01044;
                                                                                                                                                                                                     DOMAIN
ACT_SITE
ACT_SITE
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 MOCLYVLRKIGLLINLFQVTKEAVKOSFFTQPQL-ETHVLTLVNVNNNLTAKDEKRLCFI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSAEVIHOVEEALDTDEKEMLLFL---CRDVAIDVVPPNVRDLLDILRERGKLSVGD--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE-95277837; PubMed-7538907;
Chinnalyan A.M., O'Rourke K., Tewarl M., Dixit V.M.;
FADD, a novel death domain-containing protein, interacts with the death domain of Fas and initiates apoptosis.";
Cell 81:505-512(1995).
   E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 MKDYMGRGKISKEK --- SFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDL 164
                                                                                                                                                                                                                                                                                        genetic
C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FADD_HUMAN STANDARD; PRT; 208 AA: 013158; 014866; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 34). Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) FADD protein (FAS-associating death domain-containing protein) (Mediator of receptor induced toxicity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 109.5; DB 1; Length 167; 24.4%; Pred. No. 0.25; view 35; Mismatches 76; Indels 19
                                                                                                                                                                                                                                                                 of
                                                                                                                                                  rimary structure of the herpesvirus saimiri genome."; Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4563764212070BB9 CRC64;
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22 57

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L NATURE 392:941-945(1998).

C. CASPASE-10 TO THE ACTIVATED FAS (CD95) OR THER-1 RECEPPORS. THE CASPASE-10 TO THE ACTIVATED FAS (CD95) OR THER-1 RECEPPORS. THE RESULTING AGGREGAME CALLED THE DEATH-INDUCING SIGNALING COMPLEX.

C. INTIMERS THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) WITH CFLAR.

-1- SUBUNIT: INTERACES WITH CFLAR.
-1- SUBUNIT: INTERACES WITH CFLAR.
-1- SUBUNIT: INTERACES WITH CFLAR.
-1- SUBUNIT: OF THE SIGNAL REVOUTES.

C. 1- DOMAIN: CONTAINS A DEATH DOWAIN INVOLVED IN THE BINDING OF THE CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.

C. 1- SIMILARITY: CONTAINS 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelib-sib.ch).
                                                                                                                                                                                                                Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Both of the colling R.C., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuk S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.M., McKennan R.J., Mallek J.A., Guaratane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakasley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Salaska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005039; F:death receptor-associated factor activity; TAS. GO:0008625; P:induction of apoptosis via death domain rec. .; TAS. GO:0007048; P:oncogenesis; TAS.
MEDLINE-95229578; Pubmed-7536190;
Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
                                                             "A novel protein that interacts with the death domain of Fas/APOl contains a sequence motif related to the death domain."; J. Biol. Chem. 270:7795-7798(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 1-83.
MEDDLINE-98241233; PubMed-9582077;
Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
Lenardo M.J., Fesik S.W.;
"NMR structure and mutagenesis of the FADD (Mortl) death-effector
                                                                                                                                                                              TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U24231; AAA86517.1; -.
EMBL; X84709; CAA59197.1; -.
EMBL; BC000334; AAH00334.1; -.
PIR; A56912; A56912.
PDB; 1AIW; 16 FEB-99.
PDB; 1AIX; 16 FEB-99.
PDB; 1E3Y; 06 NOV-00.
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                                                                                                                                                       SEQUENCE FROM N.A.
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LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGED-----LDKSDVS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                     5 VIHOVEEALDTDEKEMLLFLCRDVA----IDVVPPNVRDLLDILRERGKLSVGD---LAE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEATAIN-CLIP 11262 / Serovar 6a;

MEDLINE-21537279; PubMed=11679669;

A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Chetouani F., Couve E., de Darivar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Darivar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Darivar A., Dusaurget O.,

Bentian K.-D., Fsihi H., Garcia del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hauf J., Jackson D.,

Jones L.-M., Raerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Nadueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                V->N: NO INTERACTION WITH FAS RECEPTOR. G -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
RPOC OR LIN0286.
                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                           Length 208;
                                                                                                                                                                                                                                                                                                                                                             Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                               81
23279 MW; 0E65E2F852E83507 CRC64;
                                                                                                                                                                                                                                                                                                                                                           9.4%; Score 105; DB 25.8%; Pred. No. 0.67. tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1201 AA
                                                                                                                                                  DEATH.
                                                                                  PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50168; DED; 1.
            InterPro; IPR001875; DED. Pfam; PF00531; death; 1. Pfam; PF01335; DED; 1. SMART; SM00005; DEATH; 1. SMART; SM0031; DED; 1.
InterPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 25.89
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                      Apoptosis; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 ARDLQNRSGA 192
                                                                                                                                                                                                                                                                                                                             208 AA;
                                                                                                                                                97
121
32
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P77879;
                                                                                                                                                                MUTAGEN
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I ------FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 VVGPNLKMYQCGLPKEMALELFKPFVMKELVGRGLAHNIKS-----AKRKIERMAPEIW 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVLEEVIREHPVLLNRAPTLHRLG----IQAFEPTLVEGRAIRLHPLVCTAYNADFDGDQ 454
                                                                                           SERAIN-ATCC 33090 / DSM 20649 / NCTC 11288 / Serovar 6a;
STRAIN-ATCC 33090 / DSM 20649 / NCTC 11288 / Serovar 6a;
Morse R., Collins M.D., Balsdon J.T., Reading S., Richardson P.T.;
"Cloning part of the rpoc gene encoding the B' subunit of the DNA-
dependent RNA polymerase from some Gram-positive bacteria and
comparative amino acid sequence.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: DNA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRIL------KMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              {RNA}(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLLEKCLK-----TSYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------NVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGN 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.2%; Score 103; DB 1; Length 1201; 20.3%; Pred. No. 6.6; Live 47; Mismatches 62; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           774 774 L -> S (IN REF. 2).
1201 AA; 134754 MW; 52876C3776033DBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; DNA-directed RNA polymerase; Transcription;
"Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listilist: Lindo286; -.
Listilist: Lindo286; -.
InterPro; IPR00722; RNA_pol_A.
InterPro; IPR007080; RNA_pol_Epbl_1.
InterPro; IPR007066; RNA_pol_Rpbl_3.
InterPro; IPR007083; RNA_pol_Rpbl_4.
Pfam; PF04997; RNA_pol_Rpbl_1.
Pfam; PF04997; RNA_pol_Rpbl_2; IPFam; PF04999; RNA_pol_Rpbl_2; IPFam; PF04999; RNA_pol_Rpbl_2; IPFam; PF04999; RNA_pol_Rpbl_3; IPFam; PF04999; RNA_pol_Rpbl_4; IPFam; PF04999; RNA_pol_Rpbl_5; IPFAM; SNAO0663; RPOLA_N, IPFAM; IPFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL596164; CAC95519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X89229; CAA61513.1;
PIR; AG1468; AG1468.
HSSP; Q9KWIK.
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                                                                                                                                                                                                                                                                                                                                                                                                 SUBSTRATES
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Glaser P., Frangeul L., Buchleser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Ababit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez Bernal G., Duchaud E., Durant L., Dussurget O.,
A Entian K.-D., Fsili H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T.; Hauf J., Jackson D.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Warquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
T. "Comparative genomics of Listeria species.";
C. I- FUNCTION: DNA PUEDERDERNER RNA POLYMERASE CHARIZES THE TRANSCRIPTION
C. I- FUNCTION: DNA PURPER RNA POLYMERASE CHARIZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial
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                                                      28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase APOC OR LMO0259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {RNA}(N).
-i- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
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; Pred. No. 6.6;
47; Mismatches 62; Indels 12:
                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
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PRT; 1201 AA.
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InterPro; IPR007080; RNA_pol_Rpbl_1.
InterPro; IPR007066; RNA_pol_Rpbl_3.
InterPro; IPR007081; RNA_pol_Rpbl_4.
InterPro; IPR007081; RNA_pol_Rpbl_5.
InterPro; IPR005592; RNA_pol_Rpbl_5.
Pfam; PF04897; RNA_pol_Rpbl_1; I.
Pfam; PF04893; RNA_pol_Rpbl_1; I.
Pfam; PF04893; RNA_pol_Rpbl_3; I.
Pfam; PF048093; RNA_pol_Rpbl_3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21537279; PubMed-11679669;
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STANDARD;
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                                                                                                                                                                                                                                                                          Listeria monocytogenes.
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 1201 AA
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1639;
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Pfam; PF04998; RNA_pol_Rpb1_5; 1. SMART; SM00663; RPOLA_N; 1.

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344
                                                                                                                             : ||: ||: ||: 345 VVGPNLKMYQCGLPKEMALELFKPFVMKELVGRGLAHNIKS-----AKRKIERMAPEIW 398
                                                          RKAVE------THLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL 112
                                                                                                                                                                                                                         int. J. Syst. Bacteriol. 46:1004-1009(1996).
-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                          289 QEAVDALIDNGRRGRPVTGPGNRPLKSLSHMLKG----KQGRFRQNLLGKRVDYSGRSVI
                                                                                                                                                                                                   DLLEKCLK------TSYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJES-97016803; PubMed-8863429;
Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
"Analysis of the beta' subunit of DNA-dependent RNA polymerase does
not support the hypothesis inferred from 16S rRNA analysis that
Oenococcus oeni (formerly Leuconostoc oenos) is a tachytelic
(fast-evolving) bacterium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY
                                                                                                                                                                                                                                                                        184 ------NVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGN 218
                                                                                                                                                                                                                                                                                             Leuconostoc pseudomesenteroides.
Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
NCBI_TaxID=33968;
                                                                                                                                                                                                                                                                                                                                                                                                  989 AA.
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InterPro; IPR007080; RNA_pol_Rpbl_1.
InterPro; IPR007066; RNA_pol_Rpbl_3.
InterPro; IPR007083; RNA_pol_Rpbl_4.
InterPro; IPR007081; RNA_pol_Rpbl_5.
InterPro; IPR006592; RNA_pol_Rpbl_5.
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Pfam; PF00623; RNA_pol_Rpbl_2; 1
Pfam; PF04983; RNA_pol_Rpbl_3; 1
Pfam; PF05000; RNA_pol_Rpbl_4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 37, Created)
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SEQUENCE FROM N.A.
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P94899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure, ligand binding, and localization of the human type 3 inositol 1,4,5-trisphosphate receptor expressed in intestinal epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IP3T_HUMAN STANDARD; PRT; 2671 AA. (014573; 014649; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 10-FEB-2003 (Rel. 41, Last annotation update) Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-trisphosphate receptor (Type 3 Insp3 receptor) (IP3 receptor isoform
                                                                                                                                                                                                202 LKRLLDLNAPGI---IVQN----EKRMLQEAVDALIDNGRRGRPVAGPGNRPLKSLSHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         116 MKDYMGRGK---ISKE----KSFLDL--VVELEKLNLVAPDQLDLLEK-CLKNIHRIDL
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hasegawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of human type 2 and type 3 inositol 1,4,5-trisphosphate receptors."; Recept. Channels 2:9-22(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY: EXPRESSED IN INTESTINAL CRYPT AND VILLUS
                                                                                                                                                 37;
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Yamamotor Hino M., Sugiyama T., Hikiti K., Mattei M.-G., Hasegav
Sekine S., Sakurada K., Miyawaki A., Furuichi T., Hasegawa M.,
Mikoshiba K.;
                                                                                                             8.9%; Score 99.5; DB 1; Length 989; 21.6%; Pred. No. 9.5; tive 50; Mismatches 76; Indels 3
                                                                                                                                                   Indels
                                Transferase; DNA-directed RNA polymerase; Transcription
                                                              989 989
989 AA; 109914 MW; 55B1CD8CA8739D06 CRC64;
                                                                                                                                                                                                                                           LKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKS----
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                                                                                                                                                                                                                                                                                                                                                                        165 KTKIQKYKQSVQGAGTSYRNVLQAAIQK 192
                                                                                                                                                                                                                                                                                                                                                                                              314 AGNVKSAKRKIDKADGDVMDVLEDVIKE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94117432; PubMed-8288584;
                                                                                                                                                 Conservative
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nes 45; Conserv
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 HLLRNPHLVSDYRVLMAEIGEDLDKSD-VSSLIF----LMKDYMGRGKI-----SK 127
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; Pred. No. 31;
52; Mismatches 73; Indels (
                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
-1 - SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                     transport; Calcium channel.
202 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                           A -> V (IN REF. 2).
H -> Y (IN REF. 2).
H -> Y (IN REF. 2).
A -> T (IN REF. 2).
L -> V (IN REF. 2).
T -> PV (IN REF. 2).
L -> V (IN REF. 2).
V -> V (IN REF. 2).
V -> V (IN REF. 2).
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                                                                                                                           MIM; 147267; -...
InterPro; IPR000699; Ca-rel_channel.
InterPro; IPR001689; Ca/Na_Pore.
InterPro; IPR005821; Ion_trans.
InterPro; IPR003608; MIR.
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                                                                                         EMBL; D26351; BAA05385.1; -. EMBL; U01062; AAC50064.1; -.
                                                                                                                                                                       Pfam; PF00520; 10n_trans; 1.
Pfam; PF02815; MIR; 4.
Pfam; PF01365; RYDR_ITPR; 2.
SMART; SM00472; MIR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
1 Similarity 20.3%;
47; Conservation
                                                                                                           PIR; A49873; A49873.
Genew; HGNC:6182; ITPR3.
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AEDLINE-2115621; PubMed-11258796; MEDLINE-2115621; PubMed-11258796; MEDLINE-2115621; PubMed-11258796; MEDLINE-2115621; PubMed-11258796; MEDLINE-2115621; PubMed-11258796; Marata T., Takino K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence Of enterohemorrhagic Escherichia coli COMPANIA AND GENERAL SECHERICHIA COLI CONTRA AND MARKA AND MARK
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MEDLINE-22388234; PubMed-12471157;
WEICH RA., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liouu S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=KLZ - MG1625.
STRAIN=KLZ - MG1627.
STRAIN=KLZ - MG1627.
STRAINE-974.2617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Greepr J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Greepr J., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562, 217992, 83334;
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MEDLINE-21074935; Pubmed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
19ptothetical protein yolM precursor.
YCIM OR B1280 OR C1749 OR 22526 OR ECS1853.
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Hidaka M., Akiyama M., Horiuchi T.;
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Escherichia coli 06, and
Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 IHQTLMESASLTYEQRLLAIQQLGRDYMAAGLYDRAEDMFNQLTDETDFRIGALQQLLQI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 KSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLK 165
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063269;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-trisphosphate receptor (Type 3 Insp3 receptor) (IP3 receptor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 IHQ--VEEALDTDEKEMILF--LCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YRV----RRFDLLKRILKM--DRKAVE-THL---LRNPHLVS---DYRVLMAEIGEDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 YQATSEWQKAIDVAERLVKLGKDKQRVEIAHFYCELALQHMASDDLDRAMTLLKKGAAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     R EMBL; AE000226; AAC74362.1; -.
R EMBL; D90766; BAA14834.1; -.
R EMBL; D00765; BAA14834.1; -.
R EMBL; AE005379; AAN80215.1; -.
R EMBL; AP002556; BAB35276.1; -.
R EMBL; AP002556; BAB35276.1; -.
R EMBL; A85759; A85759.
R PIR; C64876; C64876.
R PIR; E90860; E90860.
R E00Gene; E312691; yciM.
R InterPro; IPR001440; TPR.
R Pfam; PF00515; TPR; 2.
R Pfam; Pfam; Pf00515; TPR; 2.
R 
consensus sequence of three DNA replication terminus sites on coll chromosome is highly homologous to the terR sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                   Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
HYPOTHETICAL PROTEIN YCIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 374 C4-TYPE (POTENTIAL).
389 AA; 44531 MW; F4D1B9EZA526BCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 98.5; DE
22.6%; Pred. No. 3.9;
ative 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 TKIQKYKQSVQGAGTSYRNVLQAAIQKS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE #96032851; PubMed = 7567469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 22.6 nes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITPR3.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
389
374
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                                                       Cell 55:467-475(1988)
                                                                                               IDENTIFICATION
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SEQUENCE
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DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
BINDING SITE IN THE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SVGDLAELLYRVRRFDLLKRILKMDRKAVET
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                             MEDLINE-9326659; PubMed-8388391; Beln G.I.; Beln G.I.; Blondel O., Takeda J., Janssen H., Seino S., Bell G.I.; Blondel O., Takeda J., Janssen H., Seino S., Bell G.I.; Squence and functional characterization of a third inositol trisphosphate receptor subtype, IP3R-3, expressed in pancreatic islets, kidney, gastrointestinal tract, and other tissues."; J. Biol. Chem. 268:11356-11363(1993).

J. BIOL. Chem. 268:11356-11363(1993).

HESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel.

CYTOPLASMIC (POTENTIAL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLLRNPHLVSDYRVLMAEIGEDLDKSD-VSSLIF----LMKDYMGRGKI----
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W; 13C787E4C2886E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Pred. No. 3/;
Live 52; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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PIR; A46719; A46719. ca-rel_channel.
InterPro; IPR000699; Ca-Na_pore.
InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR005821; Ion_trans.
InterPro; IPR0350; MIR.
Ffan; PF00520; ion_trans; 1.
Pfan; PF012815; MIR; 4.
Pfan; PF01385; RYDR_ITPR; 2.
SMART; SM00472; MIR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --
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Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 20.3
Matches 47; Conservative
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22264
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2670 AA;
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 -----
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Search completed: August 13, 2003, 16:40:21 Job time : 11.4579 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 13, 2003, 16:34:29; Search time 38.7775 Seconds

(without alignments)

1470.690 Million cell updates/sec
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(without alignments)
1470.690 Million cell updates/sec
Title: US-09-380-546A-4
Perfect score: 1114
Sequence: 1 MSAEVIHQVEEALDIDEKEM.....RMITPYAHCPDLKILGNCSM 221
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Gapop 10.0 , Gapext 0.5 Searched: 830525 seqs, 258052604 residues Total number of hits satisfying chosen parameters: 8305

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

 Result
 Query

 No.
 Score
 Match Length DB
 ID
 Description

 1
 1007
 90.4
 462
 4 096TE4
 O96te4
 homo saplen

 2
 718
 64.5
 218
 11
 099MZ5
 099mz5
 rattus norv

 3
 342
 30.7
 418
 13
 080VG5
 099mz5
 rattus norv

 4
 245
 22.0
 182
 12
 099Cx0
 00vine herp
 P88961
 kapps1
 sa

 5
 224
 20.1
 476
 13
 091803
 polevial
 parchydanio

 7
 208
 18.7
 482
 13
 090WJ
 091893
 parchydanio

 7
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 090WJ
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 parchydanio

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 18.0
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 11
 091864
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 coping1

 9
 177
 15.9
 500
 13
 091864
 091864
 091864
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O8mj18 macaca mula	O56959 saimiriine	P94866 leuconostoc	Q8ewp6 mycoplasma	Q81469 plasmodium	Q8bwe0 mus musculu	Q8ety7 oceanobacil	Q8svz5 encephalito	Q8wn95 bos taurus	Q85014 porcine rot		Q945s6 lycopersico	Q8pqa6 xanthomonas		. Q85015 porcine rot	054085 streptococc	Q8rz04 oryza sativ	O66656 aquifex aeo		Q8e0e6 streptococc		P95688 staphylococ				Q8ge65 corynebacte	Q82048 human rotav	Q8msbl drosophila
Q8MJ18	2 056959	P94866	.6 Q8EWP6	081469	.1 Q8BWE0	.6 QBETY7	08SV25	Q8WN95	.2 085014	.7 Q973B7	.0 094556	.6 Q8PQA6	.0 Q9C9N6	2 085015	054085	.0 Q8RZ04	959990 9	.6 Q8E620	.6 Q8E0E6	.7 Q9YDV0	P95688	.6 Q9X2F5	.6 Q99W64	.2 082053	Q8GE65	2 082048	08MSB1
78 6	167 1	772 2	801 1	979 5	1157 1	1203 1	1256 5	2664 6	313 1	399 1	1297 1	572 1	607	313 1	345 2	700	310 1	345 1	345 1	445 1	541 2	833 1	1207 1	313 1	698	313 1	394 5
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103.5	102.5	101.5	99.5	99.5	99.5	66	66	66	98.5	98.5	86	46	. 96.5	96	96	96	95.5	95.5	95.5	95.5	95	95	95	94.5	94.5	93.5	93.5
17	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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zebrafish.
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                                                                                              RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                           1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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 Length 462;
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SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
SIGNATION—Sprague-Dawley;
Axiao C.W., Asselin E., Tsang B.K.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF244366; AAK20358.1;
Interpro: IPR001875; DED.
R pfam; PF01335; DED; 2.
R PROSITE; PS50168; DED; 2.
R PROSITE; PS50168; DED; 2.
R SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;
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                                      Indels
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(Tremblrel. 17, Last sequence update)
(Tremblrel. 18, Last annotation update)
Score 1007; DB 4;
Pred. No. 1.7e-67;
1; Mismatches 0;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                               218 AA.
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   90.48;
99.58;
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Matches 148; Conservative
                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                     Similarity
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01-JUN-2001 (TrEM
01-OCT-2001 (TrEM
FLIP short form.
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     Query Match
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08UVG5;
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Matches
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LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMK 117
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                                            Darachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
CSprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed-10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified
                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98021435; PubMed=9380701;
Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
"CLARP, a death effector domain-containing protein interacts with caspase-8 and regulates apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
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Gonome Sequence of Bovine Herpesvirus 4, a Bovine Rhadinovirus,
Identification of an Origin of DNA Replication.";
J. VIrol. 75:1186-1194(2001).
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MEDLINE-20583805; PubMed-11152491;
Zimmermann W., Broll H., Ehlers B., Buhk H.-J., Rosenthal A.,
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448261; AAL41007.1;
InterPro: IPR001875; DED.
InterPro: IPR001399; ICE.
InterPro: IPR001399; ICE.
SWART; SM00115; CASC; 1.
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 342; DB 13;
41.9%; Pred. No. 9.1e-18;
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Best Local Similarity 41.9%
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Gammaherpesvirinae.
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01-OCT-2001
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61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                   Neipel F., Albrecht J.C., Fleckenstein B.; "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?"; J. Virol. 71:4187-4192(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopteryg11; Neopteryg11; Teleoste1; Ostarlophys1; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20373792; PubMed-10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQ 169
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                      21.0%; Score 234; DB 12; 34.3%; Pred. No. 4.4e-10; iive 39; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 AA
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EMBL; AF273220; AAF79207.1; -.
HSSP; Q15806; 1QDU.
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ZFIN; ZDB-GENE-000713-1; Casp8.
InterPro; IPR001875; DED.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF001335; DED; 2.
Pfam; PF00655; ICE_p20; 1.
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                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      58 LLYRVRRFDLLKRILKMDRKAVETHLLRNP-HLVSDYRVLMAEIGEDLDKSDVSSLIFLM 116
                                                                                                                                                                                                                                      2 VIRDVLLAIETHLNQNEKTFVMYFLLD---PYIPKECEDFLPTLENLHSKRKIIYPILIE 58
                                                                                                                                                              1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDL---LDILRERGKLSVGDLAE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97121480; PubMed-8962146;
Russo J.J., Bohenzky R.A., Chlen M.C., Chen J., Yan M., Maddalena D.,
Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
"Nucleoilde sequence of the Kaposi sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
Neipel F., Mattmann C., Burns K., Bodmer J.L., Schroter M.,
Scaffidi C., Krammer P. H., Peter M. E., Tschopp J.;
"Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              117 KDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYK 172
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97094184; PubMed-8939871;
MOORE P.S., Bashoff C., Welss R.A., Chang Y.;
"Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV.";
                                                                                                                                  . .
8
                                                                                                     Length 182;
                                                                                                                                  Indels
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Neipel F., Albrecht J., Fleckenstein B.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                           550168; DED; 2.
182 AA; 21792 MW; 73BF1ADD9B0FE6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             P88961.
01-MAY-1997 (TrEMBLrel. 03, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLICE inhibitory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
                                                                                                   Query Match 22.0%; Score 245; DB 12; Best Local Similarity 32.4%; Pred. No. 6.4e-11; Matches 57; Conservative 44; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97296220; Pubmed-9151804;
EMBL; AF318573; AAK07993.1; -.
InterPro; IPR001875; DED.
Pfam; PF01335; DED; 1.
SMART; SM00031; DED; 2.
PROSITE; PS50168; DED; 2.
SEQUENCE 182 AA; 21792 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 274:1739-1744(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     death receptors.";
Nature 386:517-521(1997).
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY:
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Gaps .; 8

Length 188; Indels

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LAELLYRVRRFDLLKRILKMDRKAVETHL-LRNPHLVSDYRVLMAEIGEDLDKSDVSSLI 113
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                                                                                                                                                                                                                                                                                              60 YRVRRFDLLKRILKMDRKAVETHL-LRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKD 118
                                                                          AEVIHQVEEALDTDEKEMLLFLCRD-VAI--'--DVVPPNVRDLLDILRERGKLSVGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Cerebellum;
Cao G., Graham S.H., Chen D., Chen D.,
Molecular cloning and characterization of rat caspase-8: Its
implication in delayed neuronal cell death after ischemia.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF279308; AAR87778.1; -
EMBL; AF279308; AAR8755.1; -
                                                                                                                                                                                                                                                                                                                                                                                                        174 SVQGAGTSYRNVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGNC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%; Score 201; DB 11; Length 4 31.2%; Pred. No. 3.8e-07; ive 38; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley;
Itoh T., Itoh A., Pleasure D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 AA; 55339 MW; 82B4A29330C53264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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MEROPS; C14.009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKIQKYKQSVQGAGTSY-------RNVLQAAIQKSLKDP--SNNFRMIT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DL-AELLYRVRRFDLLKRILKMDRKAVETHLLRNPHL---VSDYRVLMAEIGEDLDKSDV 109
                                                                                                                                                                                                                                                                                                                                      1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVG 53
                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLD----LLEKCLKNIHRIDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caspase 8.
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                        44;
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                                                                                                                                                                                                                                  Length 476;
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                                                                                                                                                                                                                                                                                      Indels
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Barton S., Bridgham J.T., Johnson A.L.;

"Caspase-8 and -9 expression in the hen ovary.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY059393; AAL23700.1;

MEROPS; C14.009;
                                                                                                                                                                54890 MW; FD9DFF4B3C3C1FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54645 MW; 8E3936B6EE090BEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                            20.1%; Score 224; DB 13; 28.7%; Pred. No. 7.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA
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                                                                                                                                                                                                                                                                                47; Mismatches
SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50108; CASPASE_P20; 1.
PROSITE; PS50168; DED; 2.
SEQUENCE 476 AA; 54890 MW; FD9D
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PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS50208; DS0; 2.
SEQUENCE 482 AA; S4645 MW; 8E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001875; DED.
Interpro; IPR001398; ICE.
Interpro; IPR001398; ICE.p10.
Interpro; IPR001399; ICE.p10.
Interpro; IPR01395; DED; 2.
Pfam; PP01395; DED; 2.
Pfam; PP00655; ICE.p10; 1.
Pfam; PP00655; ICE.p20; 1.
Pfam; PR00155; ICE.p20; 1.
SMART; SMO0115; CASC; 1.
                                                                                                                                                                                                                            Query Match 20.19
Best Local Similarity 28.79
Matches 71; Conservative
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                                                                                                                        119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQS 174 :: | | :: | | :: | | :: | | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20209426; Pubmed=10744739;
Nakajima K., Takahashi A., Yaoita Y.;
"Structure, expression and function of the Xenopus laevis caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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28.4%; Pred. No. 2.5e-05;
Live 44; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS0112; CASPASE CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS00255; INTERLEUKIN_7_9; 1.
SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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InterPro: IPR002398; ICE.
InterPro: IPR002398; ICE_D10.
InterPro: IPR001309; ICE_D20.
InterPro: IPR001309; ICE_D20.
InterPro: IPR00326; Interleukin_7_9.
Pfam; PP00335; DED; 2.
Pfam; PP00655; ICE_D10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.";
J. Biol. Chem. 275:10484-10491(2000).
EMBL; AD338171; BAA94749.1; -.
HSSP; Q18806; 1QDU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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01-OCT-2000 (TrEMBLrel. 15, Created)
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SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 28.44
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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NCBI_TaxID=8355;
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XCASPASE-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91B64;
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AC 099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20209426; PubMed-10744739; Nakajima K., Takahashi A., Yaoita Y.; **Structure, expression and function of the Xenopus laevis caspase
                                                                                                                                             XCASPASE-10.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 161; DB 13; Length 520; ilarity 27.5%; Pred. No. 0.00041; Conservative 34; Mismatches 57; Indels 40
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PROSITE; PSO1121; CASPASE_HIS; 1.
PROSITE; PSO2007; CASPASE_P10; 1.
PROSITE; PSS01089; DED; 2.
PROSITE; PSS0168; DED; 2.
SEQUENCE 520 AA; 59626 MW; 33164A5A09CA6615 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Caspase 10, apoptosis-related cysteine protease.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 275:10484-10491(2000).
EMBL; AB038173; BAA94751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002138; ICE_p10.
Interpro; IPR001309; ICE_p20.
Pfam; PF001355; DED; 2.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SMO0115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q15806; 1QDU.
InterPro; IPR001875; DED.
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LKIIEKYKE 174
                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002398;
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les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-FEB-1997
01-JUN-2001
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                                                                                                                                                                                          Moss B.;
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                                                                                                                                                            LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKD 118
                                                                                                                                                                              119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLE-----KCLKNIHRIDLKTKIQ- 169
                                                                                                                                                                                                                                 GMTRECAGR--LLGHGFLSOYRLQVAAINNMVGSEDLRVMC-----LCAGKLLPPSCTP 127
                                                                                                          28
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                                                                                                                                27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF
                                                                                                       9 VEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVGD---LAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
Lopez Estebaranz J.L., Esteban M., Martin-Gallardo A.;
A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Molluscipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 KSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQ--KYKQSVQGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 369;
                                                   14.4%; Score 160; DB 4; Length 522; 29.8%; Pred. No. 0.00049; Live 33; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                          58993 MW; 34847E07B3DFA688 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 369 AA; 38403 MW; FECD119A576FF001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01.JUL-1997 (TrEMBLrel. 04, Created)
01.JUL-1997 (TrEMBLrel. 04, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 38.4 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.3%; Score 159; DB 12; 29.9%; Pred. No. 0.00039; ive 26; Mismatches 80;
                                                                                                                                                                                                                                                                                   197 VTPPVDKEAESYQGEEELVSQTDVKTFLEALPQES 231
                                                                                                                                                                                                                                                                  170 -----KYKQSVQG-----AGTSYRNVLQAAIQKS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AA
                                                                                                                                                                                                                                                                                                                                                            369 AA
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EMBL; BC042844; AAH42844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus Genes 0:0-0(1997).

EMBL: U86889; AAB57924.1; -.
INTERPRO; IPRO01875; DED.
SMART: SM00031; DED: 2.
PROSITE; PS50168; DED; 2.
                                                                              64; Conservative
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NON_TER 369 36
                                                               Best_Local Similarity
Matches 64; Conserv
                          522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                            59
             Protease.
                             SEQUENCE
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                                                    Query Match
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Q98326
ID Q98326
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MEDINE-21100893; PubMed-11161814;
MEDINE-21100893; PubMed-11161814;
MEDINE-21100893; PubMed-11161814;
MAINTINGALD., Kanagisawa Y., Skaug J., Fichter K., Nasir J.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Treda J.-E., Hayden M.R.;
"Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
Tricolo-213(2001).
EMBL; AB038978; BAB32553.1; JOINED.
BREME; AB038975; BAB32553.1; JOINED.
BREME; AB038977; BAB32553.1; JOINED.
BREME; AB038977; BAB32553.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GMTRECAGR--LLGHGFLSQYRLQVAAINNMVGSEDLRVMC-----LCAGKLLPPSCTP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 KMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKI----SKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96325459; PubMed-8670425;
Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darai G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of a human tumorigenic poxvirus: Prediction of specific host response-evasion genes."; Science 273:813-816(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substituted (JUN-1996) to the EMBL/GenBank/DDBJ databases EMBL; U60315; AAC55288.1; -.
InterPro; IPR001875; DED.
SMART; SM00031; DED.
PROSITE; PRO5014; DED; 2.
SEQUENCE 371 AA; 38625 MW; 48123BADD29667AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V.,
Moss B.;
(TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%; Score 157; DB 12; 29.9%; Pred. No. 0.00056; ive 25; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                  Molluscipoxvirus.
NCBI_TaxID=10280;
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119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLE-----KCLKNIHRIDLKTKIQK 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 VEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVGD---LAEL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSASDVFEHLLAEDLLSEEDPFFLAEL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99174001; PubMed-10074154;
Searles R.P., Bergquam E.P., Axrhelm M.K., Wong S.W.;
Sequence and genomic analysis of a rhesus macaque rhadinovirus with similarity to kaposi's sarcoma-associated Herpesvirus/Human herpesvirus B.;
J. Virol. 73:3040-3053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 14.1%; Score 157; DB 4; Length 479; Similarity 29.3%; Pred. No. 0.00075; 60; Conservative 31; Mismatches 86; Indels 28;
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                                                                             | InterPro; IPRO02138; ICE_p10. |
| InterPro; IPR001309; ICE_p10. |
| InterPro; IPR001309; ICE_p10. |
| Pfam; PF00655; ICE_p10; 1. |
| Pfam; PF00656; ICE_p10; 1. |
| Pfam; PF00656; ICE_p10; 1. |
| PRINTS; PR00376; ILIBCENZYME. |
| SMART; SM00115; CASPASC, 1. |
| SMART; SM00115; CASPASC_CYS; 1. |
| PROSITE; PS01121; CASPASE_LYS; 1. |
| PROSITE; PS50207; CASPASE_P10; 1. |
| PROSITE; PS50208; CASPASE_P10; 1. |
| PROSITE; PS50168; DED; 2. |
| PROSITE; PS50168; DED; 2. |
| SEQUENCE 479 AA; 54565 MW; 1317FD7A4EE003FF CRC64;
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Gammaherpesvirinae; Rhadinovirus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 YKQSVQGAGTSYRNVLQAAIQKSLK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 VTPPVDKEAESYQGEEELVSQTDVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta rhadinovirus 17577.
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     IPR001875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 60; Conserv
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 15, Appl Sequence 22, Appl Sequence 1, Appl Sequence 17, Appl Sequence 17, Appl Sequence 2, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 318, Appl
SUMMARIES	US-09-410-194-15 US-09-410-194-22 US-09-410-194-22 US-09-410-194-11 US-09-410-194-17 US-09-410-194-17 US-09-410-194-12 US-09-410-194-12 US-09-410-194-19 US-100-005-921-2 US-100-105-921-2 US-100-105-921-2 US-100-105-928-37 US-100-105-928-37 US-100-105-928-37 US-09-009-893-6 US-09-01015-928-37 US-09-01015-928-37 US-09-01015-928-37 US-09-01015-928-37
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Query Match 100.0%; Score 1114; DB 9; Best Local Similarity 100.0%; Pred. No. 3e-101; Matches 221; Conservative 0; Mismatches 0;

ORGANISM: Homo sapiens

SEQ ID NO 15 LENGTH: 221 TYPE: PRT US-09-410-194-15

1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

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Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 18, Appli Sequence 190, Appli Sequence 190, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli	
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Query Match
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Similarity 100.0%; Pred. No. 3e-101;
21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.
PRIOR FILING DATE: 1997-04-01
SOFTWARE: FASTESO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                              Sequence 22, Application US/09410194
Patent No. US20020095030A1
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US-09-861-270-2
; Sequence 2, Application US/09861270
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Rimoldi, Donata
Hofmann, Kay
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Schneider, Pascal
Bodmer, Jean- Luc
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Hahne, Michael
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APPLICANT: Thome, Margot
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Matches 221; C
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LENGTH: 221
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1 MSAEVIHQVEEALDTDEKEMLIFICKBVAIDVVPPNVRDLLDILKERGKLSVGDLAELLY
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                            ADDRESSEE: Science & Technology Law Group STREET: 75 Denise Drive CITY: Hillsborough STATE: California COUNTRY: USA ZIP: 94010 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.4%; Score 1007; DB 9; 99.5%; Pred. No. 2.6e-90; tive 1; Mismatches 0;
                                            APPLICANT: Sul, Hong-Bing
Goeddel, David V.
TITLE OF INVENTION: Regulators of Apoptosis
CORRESPONDENCE: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/861,270
FILING DATE: 18-May-2001
CIASSIFCATION SCHOON
PRIOR APPLICATION NUMBER: 08/795,088
FILING DATE: CONDON:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAIN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (550),343-4141
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-861-270-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SYRNVLQAAIQKSLKDPSNNFRM 203
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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Patent No. US20020095030A1
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 480 amino acids
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APPLICANT: Tschopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Irmler, Marten
APPLICANT: Hahne, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Patent No. US20020052474A1 GENERAL INFORMATION:
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US-09-410-194-11
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TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                   61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                   Gaps
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                                                             Length 480;
                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
                                                        Score 1007; DB 9;
Pred. No. 2.6e-90;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            181 SYRNVLQAAIQKSLKDPSNNFRM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: N. JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                        Query Match
Best Local Similarity 99.5%;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 480 amino acids
amino acid
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  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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ORGANISM: HOI US-09-410-194-17
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Pred. No. 2.6e-90;
1; Mismatches 0; Indels
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TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 1114-1002014
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: OFT/EP98/01857
PRIOR PILING DATE: 1998-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FSSLEEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                        APPLICANT: French. E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/FP98/01857
PRIOR PILING DATE: 1998-03-31
PRIOR PLING DATE: 1999-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYRNVLQAAIQKSLKDPSNNFRM 203
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                Bodmer, Jean- Luc
Steiner, Veronique
Rimoldi, Donata
Hofmann, Kay
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Best Local Similarity 99.5%;
Matches 202; Conservative
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Rimoldi, Donata
Hofmann, Kay
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Schneider, Pascal
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Burns, Kimberly
Irmler, Marten
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                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-410-194-11
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 11
LENGTH: 480
                                                                         APPLICANT:
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                APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
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       0; Gaps
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       0; Indels
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Best Local Similarity 74.5%; Pred. No. 1.6e-61;
Matches 146; Conservative 19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
       1; Mismatches
                                                                                                                                                                                                                                                                       181 SYRNVLQAAIQKSLKDPSNNFRL 203
                                                                                                                                                                                                                                                  181 SYRNVLQAAIQKSLKDPSNNFRM 203
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Rimoldi, Donata
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APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean- Luc
     202; Conservative
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Hahne, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                Thome, Margot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-09-410-194-12
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          .09-410-194-12
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LENGTH: 481
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                                                                                                                           1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPDNVRDLLDILRERGKLSVGDLAELLY

MSAEVIHQVEEALDTGEKEMLLFLCRDVAIDVVPDNVRDLLDILRERGKLSVGDLAELLY
                                                                                                        1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                         Gaps
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                                      Length 480;
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                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09471749
Publication No. US20030124113a1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Rail C.
APPLICANT: Guegler, Rail J.
APPLICANT: Baughn, Mariah
TITLEO F INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1007; DB 11;
Pred. No. 2.6e-90;
                                 Score 1007; DB 11
Pred. No. 2.6e-90;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: US/09/471,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0519 US
                                                                                                                                                                                                                                                                                                                   181 SYRNVLQAAIQKSLKDPSNNFRM 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 3, C.
REFERENCE/DOCKET NUMBER: PF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                  Query Match 90.4%;
Best Local Similarity 99.5%;
Matches 202; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THP1PLB02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-09-009-893-2
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-471-749-1
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STATE:
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; LOCATION: (97)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318
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                                                                                                                                                                                                                                                                                                                                                    RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL---MK 117
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                                                                                                                                                                                                                                                        1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                             Gaps
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                                                                                                  Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 391;
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Publication No. US20030092615A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PIZO4C1
CURRENT APPLICATION NUMBER: US/10/115,928
CURRENT FILING DATE: 2002-04-05
PILOT APPLICATION NUMBER: CS CONTRACT OF SEQUENCE OF SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 318
LENGTH: 391
                                                                                                                                                         Indels
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                                                                                        63.0%; Score 701.5; DB 14; 73.4%; Pred. No. 2.2e-60; Live 19; Mismatches 29; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 318, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | ||::| |:|
186 A-RSNMNTLQASLPKLSIK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 AGTSYRNVLQAAIQK-SLK 195
                                                                                           Query Match 63.0%,
Best Local Similarity 73.4%,
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (97)
; ORGANISM: Mus musculus US-10-005-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-10-103-313-318
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; Pred. No. 1.6e-61;
19; Mismatches 29; Indels
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Sequence 2, Application US/10005921
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
TITLE OF INVENTION: DISRUPTIONS
FILE REFERENCE: P.714
CURRENT APPLICATION NUMBER: US/10/005,921
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,902
PRIOR FILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: RestSEQ for Windows Version 4.0
                                                                                                                                                                                                                                 APPLICANT: Inniber: Matten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Pascal
APPLICANT: Budmer, Jean-Luc
APPLICANT: Rimoldi, Donata
APPLICANT: Rrench, E. Lars
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: Hofmann, Kay
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FILP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 27
SOCTHWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%; Score 713; 74.5%; Pred. No. 1
                                                       Sequence 19, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
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                                                                                                                                                                                   Thome, Margot
Burns, Kimberly
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                                                                                                                                                         APPLICANT: Tschopp, Jurg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
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                             US-09-410-194-19
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LENGTH: 484
TYPE: PRT
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Publication No. US2000087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: GENTZ, REINER L.
APPLICANT: GENTZ, NEINER L.
APPLICANT: GENTZ, TEINER L.
APPLICANT: GENTZ, TEINER L.
APPLICANT: APPLICANT: TEINER L.
APPLICANT: APPLICANT: NEINER L.
APPLICANT: APPLICANT: OS TONOREL INHIBITOR OF TUMOR
TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                         ; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-115-928-37
                                                                                                                                                                                                                                                                                            95 VLMARIGEDLDKSDVSSLIFTAKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEK 154
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                                                                                                                                                                                                                                                                                                                                                                            155 CLKNIHRIDLKTKIQKYKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRM 203
                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
                                                                                                                                                                                                                                                     Indels
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CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009, 893
                                                                                                                                                                                                            Score 532; DB 15;
Pred. No. 6.4e-44;
1; Mismatches 1;
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REGISTRATION UNDBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-3AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                          47.8%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEO ID NO: 6: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.2°
Matches 107; Conservative
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                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                   NAME/KEY: misc_feature
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US-09-009-893-6
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SEQ ID NO 37
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Pank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
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                                          Length 348;
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PRIOR FILING DATE: 2001-01-30
PRIOR PRING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2010-06-30
PRIOR PILING DATE: 2010-06-30
PRIOR FILING DATE: 2010-06-30
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OTHER INFORMATION: MAP TO AC007272.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8
                                Score 527; DB 11;
Pred. No. 1.7e-43;
0; Mismatches 0;
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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Patent No. US20020048763A1
47.3%; Scc.
100.0%; Prev
0; }
                                                                                                                                           Conservative
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                                                                                al Similarity
106; Conserv
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LENGTH: 93
                                Query Match
Best Local S
Matches 106
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58 LLYRVRRFDLLKRILKMDRKAVETHLLRNP-HLVSDYRVLMAEIGEDLDKSDVSSLIFLM 116
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                                                                                                                                                                                                                                                                                                                                                              1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDL---LDILRERGKLSVGDLAE 57
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OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.0
OTHER INFORMATION: SWISSPROT HIT: 066674, EVALUE 3.00e-04
OTHER INFORMATION: EST_HUMAN HIT: W23795.1, EVALUE 2.00e-46
                                                                                                                                                                                                                                                           41.7%; Score 465; DB 9; Length 93; 100.0%; Pred. No. 3.4e-38; Live 0; Mismatches 0; Indels
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TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCI/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09410194 Patent No. US20020095030A1 GENERAL INFORMATION: APPLICANT: Tschopp, Jurg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bovine herpesvirus 4 US-09-410-194-24
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Rimoldi, Donata
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Schroter, Michael
Schneider, Pascal
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Matches 93; Conserva
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CTHER INFORMATION:
US-09-864-761-36370
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Search completed: August 13, 2003, 16:56:03 Job time: 24.0143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 13, 2003, 16:36:59; Search time 16.0785 Seconds (without alignments) 1321.848 Million cell updates/sec Run on:

1 MSAEVIHQVEEALDTDEKEM......RMITPYAHCPDLKILGNCSM 221 US-09-380-546A-4 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283308 Total number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pik_76:*
1: pirl:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description ,	hypothetical prote	_	_			hypothetical prote		RNA polymerase (be	RNA polymerase (be	inositol 1,4,5-tri		pr	heat	ı	inositol 1,4,5-tri	RNA polymerase (be		histidine kinase s	hypothetical prote	maltose ABC transp	RNA polymerase bet	NSP3 protein - hum	laminin gamma-1 ch	NSP3 protein - hum	myosin heavy chain	RNA	RNA		DNA-directed RNA p
SUMMARIES	ΩI	T30761	S55668	T30762	E36813	A56912	T31008	T09641	AD1107	AG1468	A49873	S51753	C64876	E90860	A85759	A46719	669698	S51754	D70328	E72674	H72205	A89822	S51730	MMFFB2	S51725	A37352	T10432	T10908	C82007	F81233
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ď	Query	19.6	15.3	_				9.5								8.8	8.7	9.6	8.6	9.6	8.5	8.5	8.5	8.4	8.4	8.3	8.3	8.3	8.3	8.3
	Score	218.5	170.5	157	109.5	105	103.5	103	103	103	66	98.5	98.5	98.5	98.5	98	97	96	95.5	95.5	95	σ	94.5	0	93.5	93	93	93	92.5	92.5
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hypothetical prote probable nuclear p	casein kinase II (probable sigma fac	conserved hypothet hypothetical prote	nonstructural prot hypothetical prote protein g377 - mal	casein kinase (EC nonstructural prot coenzyme POO synth	DNA-directed RNA p exodeoxyribonuclea DNA-directed RNA p
T29145 T41023	S20404 B96919	AD0655 B96834	MNAKBK T31555 T18414	149141 S51769 E90347	T09645 H70178 T44376
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ALIGNMENTS

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N.Alternate names: RAS-associating death domain containing protein FADD; mediator of C; Species: Homo sapiens (man)
C; Accession: A56912; 138041
R; Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.
C; Accession: A56912; 1995
A; Title: FADD, a novel death domain-containing protein, interacts with the death doma A; Reference number: A56912; MUID:95277837; PMID:7538907
A; Scteus: preliminary
A; Accession: A56912
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-208 cCHI>
A; Cross-references: GB:1024231; NID:9809486; PIDN:AAA86517.1; PID:9809487
B; Boldin, M.P.; Varfolomeev, E.E.; Pancer, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D. J. Biol. Chem. 270, 7795-7798, 1995
A; Title: A novel protein that interacts with the death domain of Fas/APO1 contains a A; Accession: TabAA1
R; Nicholas, J.; Cameron, K.R.; Honess, R.W.

Nature 355, 362-365, 1992

A; Title: Herpesvirus saimiri encodes homologues of g protein-coupled receptors and cy
A; Reference number: $20243; MUID:92115001; PMID:1309943

A; Accession: A58939

A; Accession: A58939

A; Residues: 1-61 < AIC.>
A; Cross-references: GB:S76368; NID:9243351; PIDN:AAB21118.1; PID:9243355

A; Cross-references: GB:S76368; NID:9243351; PIDN:AAB21118.1; PID:9243355

B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;
A; Virol. 66, 5047-5058, 1992

A; Virol. 66, 5047-5058, 1992

A; Title: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A37309; MUID:92333688; PMID:1321287

A; Contents: annotation; protein-coding frames
A; Note: neither protein nor nucleotide sequence is given
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSAEVIHQVEEALDTDEKEMLLFL---CRDVAIDVVPPNVRDLLDILRERGKLSVGD--L 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1.31,'V',33-208 <RES>
A;Cross.references: EMBL:X84709; NID:g791037; PIDN:CAA59197.1; PID:g791038
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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25.8%; Pred. No. 1;
iive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.8%; Score 109.5; Di
Best Local Similarity 24.4%; Pred. No. 0.36;
Matches 42; Conservative 35; Mismatches
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C;Superfamily: receptor-induced
C;Keywords: aboptosis
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Best Local Similarity 25.8%
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 160L - Molluscum contagiosum virus 1
N;Alternate names: Mc160L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C;Accession: T30762
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30762
A;Accession: T30762
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                 A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13862.1; PID:g695247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: equine herpesvirus 2 hypothetical protein E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMDRKAVETHILRNPHLVSDYRVIMAEIGEDLDKSDVSSLIFILMKDYMGRGKI----SKE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GMTRECAGR--LLGHGFLSQYRLQVAAINNMVGSEDLRVMC-----LCAGKLLPPSCTP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL----MKDYMG 121
                                                                                                                                                                                                                                                                                                                                                                            65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: saintiine herpesvirus 1
Cispecies: saintiine herpesvirus 1
Cispecies: saintiine herpesvirus 1
Cispecies: saintiine herpesvirus 16-Oct-1992 #text_change 08-Oct-1999
Cispecies: saintiine herpesvirus 1992 #text_change 08-Oct-1999
Rialbrecht, J. submitted to the EMBL Data Library, January 1992
Albecht of the EMBL Data Library, January 1992
Albecht on the EMBL and the herpesvirus saintii genome.
Albecht on 1998 # Albecht of the herpesvirus saintii genome.
Albeche type: DNA
Albecht on 1997 * Albecht of the herpesvirus 1997 * Albecht of the
                                                                                                                                                                                                                                                                                                                                                                     12 ALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLLDILRERGKLSVGDLAELLYRVRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDEDETETYLYLCRDLL----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: X64346; NID: 960320; PIDN: CAA45694.1; PID: 960392
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                                                                                                                                                                                                                          Length 171;
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hypothetical protein ORF71 - saimiriine herpesvirus 1 (strain 11)
C;Species: saimiriine herpesvirus 1
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08
C;Accession: E36813; A58939
R;Albrecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 371;
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                                                                                                                                                                                    Score 170.5; DB 2; Lengum. Pred. No. 1.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <SEN>
                                                                                                                                                                                            Cross-references: EMBL:U60315; PIDN:AAC55288.1 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Conservative
                                                                                                                                                                                                                                                                                                55; Conservative
                                                                                                                                                                                                                   Query Match
Best Local Similarity
A; Molecule type: DNA A; Residues: 1-171 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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A; Note: MC160L
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Best Local S
Matches 52,
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Qy 58 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVS 110 bb :	Genetics: Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain Keywords: nucleotidyltransferase; transcription Duery Match Ouery Match 9.2%; Score 103; DB 2; Length 1053; Best Local Similarity 20.3%; Pred. No. 10; Best Local Similarity 47; Mismatches 62; Indels 122; Gaps 30 IDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRIL
RESULT 6 T31008 hypothetical protein 422 - Sulfolobus sp. plasmid pNOB8	DD 231 LPVIPPEIRPMVQLEGGRFATSDLNDLYRRVINRNNRLKRLLDLGAPNIIVQNEKRML 288 Qy 76 RKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSL 112 :: : : : 1 : Db 289 QEAVDALIDNGRRGRPVTGPGNRPLKSLSHMLKGKQGRFRQNLLGKRVDYSGRSVI 344
C;Species: Sulfolobus sp. C;Species: Sulfolobus sp. C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: T31008 R;Shb. Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.	Qy 113 IFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDOL 149 :
Extracopnizes 1, 417-425. 1998 A; Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an A; Reference number: 220959; MUID:99044580; PMID:9827331 A; Reference number: 220959; MUID:99044580; PMID:9827331 A; Accession: T31008 A; Accession: T31008 A; Repairus: preliminary: translated from GB/EMBL/DDBJ A; Residues: 1-422 <she> A; Residues: 1-422 <she> A; Residues: 1-422 <she> A; Cross-references: EMBL:AJ010405; NID:e1351926; PID:e1351930; PIDN:CAA09114.1</she></she></she>	OY 150 DLLEKCLK
Genome: plasmid pNOB8 Ouerv Match 9.3%:	RESULT 8 AD1107 RNA nolymerase (heta) chain) (imported) - Listeria mononutonenes (ettain pon.c)
Similarity 25.0%; Pred. No. 3.1; 2; Conservative 40; Mismatches 77; Indels VIHQVEEALDTDEKEMLFLCRDVAIDVVPPNVRDLLDILR: :::: : : : : : : :	Arm Polymetase (beta chain) fillported) - Listeria Monocytogenes (strain EdD-e) C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: AD1107 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Faihl, D.: Jones, L.M.; Rarst, U
6 4	Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species. A;Reference number: AR107: MITD: 7151779.
QY 99 EIGEDLDKSDVSSLIFLMKDYMGRGKISKEK 129	A; Accession: All107 A; Status: preliminary A; Molecule type: DNA
Qy 130 SFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIOKYKOSVQGAGTSYRNVLQAA 189 :	A; Kestudes: 1-LOI COLANA A; CESSI-Teferences: GB:NC_003210; PIDN:CAD00786.1; PID:g16409624; GSPDB:GN00177 A; Experimental source: strain EGD-e C; Genetics: A; Gene: TpOC C; Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
ļ	Query Match 9.2%; Score 103; DB 2; Length 1201; Best Local Similarity 20.3%; Pred. No. 12; Matches 59; Conservative 47; Mismatches 62; Indels 122; Gaps 15;
RESULT 7 T09641 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Listeria innocua (fragment) C;Species: Listeria innocua C;Species: R:; Collins, M.D.; Balsdon, J.T.; Reading, S.; Richardson, P.T. R;Morse, R:; Collins, M.D.; Balsdon, J.T.; Reading, S.; Richardson, P.T. A;Description: Cloning part of the rpoC gene encoding the B' subunit of the DNA-dependen A;Reference number: 216792 A;Reference number: 216792 A;Residues: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1053 <anor> A;Residues: 1-1053 <anor> A;Experimental source: strain NCTC 11288</anor></anor>	

HCPDLKILGN 218 C; Superfamily: inositol-trisphosphate receptor :: -sQDM-VLGN 499 Best Local Similarity 20.3%; Pred. No. 62; Matches 47; Conservative 55; Mismatches 71; Indels	Oy 1 MSAEVIHQVEEA-LDTDEKEMLLFLCRDVAIDVV	Qy 83 ILRNPHLVSDYRVLMAEIGEDLDKSD-VSSLIFIMKDYMGRGKISKE	RESULT 11 S51753 NSP3 protein - porcine rotavirus (strain OSU) N/Alternate names: NS34 protein C;Species: porcine rotavirus A;Variety: strain OSU C;Bate: 19-Mar-1997 #sequence_revision 19-Mar-197 #sequence_revision 19-Mar-195; R;Rao, C.D.; Das, M.; Rao, B.S.; Gowda, K.	75 Subartree number: \$51709 A; Accession: \$51753 A; Molecule type: genomic Rb A; Molecule type: genomic Rb A; Residues: 1-313 cRao> A; Cross-references: EMBL:X6 A; Experimental source: stra 344 C; Superfamilly: rotavirus n	LDLVVELEKINLVAPDQL 149 : : :AKRKIERMAPEIW 398TSYR 183 : : RLHPLVCTAYNADFDGDQ 454	QY 95 VLMAEIGEDLDK 1:: :: Db 93 T-VAKLDEDVNKLRMILSS:	Qy 125 ISKEKSFLDLVVELEKLALVAPDQLDLLEKCLKNIHRIDLKTKI-OKYKQSVQGAGTSYR in 1 1	RESULT 12 C64876 VolM protein precursor - Escherichia coli (strain K-12) C; Species: Escherichia coli C; Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_ C; Accession: C64876
184NVLQAAIQKSLKDPSNNFRMITPYA : :: 455 MAVHVPLSAEAQAEARIIMLAAQNIL-NPKDGKPVVTP	RESULT 9 ANA POLYMERASE (beta' chain) [imported] - Listeria innocua (strain C;Species: Listeria innocua C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14 C;Accession: AG1468 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F. C; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; E.	D.; Jones, L.M.; Karst, U. Science, L.M.; Karst, U. Science, P., W.; P., Science, P.; Science, C.; Madueno, E.; A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoss, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Ratus: preliminary A; Molecule type: DNA	Residues: 1-1201 (GLA> Cross-references: GB.AL592022; PIDN:CAC95519.1; PID:g Experimental source: strain Clip11262 Genetics: Gene: rpoC Superfamily: Escherichia coli DNA-directed RNA polyme Query Match Best Local Similarity 20.3%; Score 103; DB 2; Le Best Local Similarity 20.3%; Pred. No. 12; Matches 59; Conservative 47; Mismatches 62;	30 IDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRIL	113 I	184NVLQAAIQKSLKDPSNNFRMITPYAHCPDLKILGN 218 	RESULT 10 A49873 inositol 1,4,5-triphosphate receptor, type 3 - human C;Specias: Homo sapiens (man) C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #tex C;Accession: A49873 R;Maranto, A.R.	J. BLOL. CORM. 209, 1222-1230, 1994 A; Title: Primary Structure, ligand binding, and localization of the A; Reference number: A49873; MUID:94117432; PMID:8288584 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-2671 < MAR> A; Cross-references: GB:U01062; NID:9453367; PIDN:AAC50064.1; PID:9399

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C.A.; Perna, N.T.; Burland, V.; Riley, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SDVSSLIFLMKDYMGRGK 124
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ches 58; Indels 65; Gaps
                                                                                                                                                                                                          KNIHRID--LKTKIQKYKQSVQ 176
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T.DPKNSDILIRTELRPVKEMAQ 678
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probable heat shock protein yciM [imported] - Escherichia coli (strain 0157:H7, subst C; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (c; Accession: A85759 (c; Accession: A85759 (c; Accession: A85759 (c; Byterna, N.T.; Plunkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousls, K.; Apoda Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-389 <STO>
A;Cross-references: GB:AE005174; NID:g12515512; PIDN:AAG56533.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inositol 1,4,5-trisphosphate receptor subtype 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A46719
R;Blondel, O.; Takeda, J.; Janssen, H.; Seino, S.; Bell, G.I.
J. Biol. Chem. 268, 11336-11363, 1993
A;Rille: Sequence and functional characterization of a third inositol trisphosphate JA;Reference number: A46719; MUID:93266594; PMID:8388391
A;Accession: A46719
A;Accession: 
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C;Superfamily: hypothetical protein HI1223; tetratricopeptide repeat homology
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A;Experimental source: insulinoma cell line RINm5F
A;Note: sequence extracted from NCBI backbone (NCBIN:132840, NCBIP:13284;
C;Superfamily: inositol-trisphosphate receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A,Reference number: A85480; MUID:21074935; PMID:11206551
   39;
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                                                                                                                                                                      ---GKTAEWAEFLORAVEEN 279
                                                                                                      166 TKIQKYKQSVQGAGTSYRNVLQAAIQKS 193
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A85759
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A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Recession: E90860
A:Status: preliminary
A:Residues: 1-389 <-HAY>
A:Residues: 1-389 <-HAY>
A:Cross-references: GB:BA000007; PIDN:BAB35276.1; PID:g13361318; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A:Gene: ECS1853
C;Superfamily: hypothetical protein HI1223; tetratricopeptide repeat homology
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                                                                                                      A; Molecule type: DNA
A; Residues: 1-389 <BLAT>
A; Cross-references: GB:AE000226; GB:U00096; NID:92367115; PIDN:AAC74362.1; PID:92367116;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
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                                                                                                                                                                                                                                                                                              A Gene: yciM
C. Superfamily: hypothetical protein Hil223; tetratricopeptide repeat homology
C. Keywords: DNA binding; Zinc finger
F.1-16/Domain: signal sequence #status predicted <SIG>
F.11-6/Domain: signal sequence #status predicted <MAT>
F.180-213/Domain: tetratricopeptide repeat homology <TT1>
F.214-347/Domain: tetratricopeptide repeat homology <TT2>
F.357-374/Region: zinc finger CCCC motif
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22.6%; Pred. No. 6.4;
tive 44; Mismatches 78; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 389;
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: C64876 A;Status: nucleic acid sequence not shown; translation not shown
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22.6%; Pred. No. 6.4;
ve 44; Mismatches 78;
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ογ	51	51SVGDLAELLYRVRRFDLLKRILKMDRKAVET 81
qq	511	511 DENILKQIFGILKAPFRDKGGEGPLVRLEELSDQKNAPYQY-MFRLCYRVLRHSQED 566
δλ	82	82 HLLRNPHLVSDYRVLMAEIGEDLDKSD-VSSLIFLMKDYMGRGKISK 127
qq	267	: ::::::::::::::::::::::::::::::::::::
δλ	128	128 EKSFLDLVVELEKLNLVA-PDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQ 176
qq	627	627 EPRFLDYLSDLCVSNRIAIPVTQELICKCVLDPRNSDLILQTELRPVKEMAQ 678
Search c	omple	Search completed: August 13, 2003, 16:43:47

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Homo sapiens.
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Human CFLIP-L prot
Human Casper prote
1-FLICE-1 protein.
Human FIN-1. Homo
Human FLICE-1ike i
Human MACH related
FLICE-like inhibit
Usurpin-alpha poly
                                                                                                                 August 13, 2003, 16:21:28 ; Search time 82.8531 Seconds (without alignments) 919.565 Million cell updates/sec
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                                                                                                                                                                                                                                  1 MSAEVIHQVEEALDTDEKEM.......EKYYVWLQHTLRKKLILSYT 480
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              protein search, using sw model
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AAB03960
AAY67418
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AAW69229
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Gapop 10.0 , Gapext 0.5
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Usurpin-beta polyp
Human gene 9 encod
Novel human neopla
Human apoptosis re
MXIT alpha 3 polyp
Human MACH related
I-FLICE-2 protein.
MXIT-NDI polypepti
MOUSE CFLIP-L prot
FLICE-like inhibit
       Human FLIP-c prote
FLIP with detectab
Human FLIP protein
Human CLARP protei
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Mouse FLIP-c prote
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Human FLAME-1 prot
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Usurpin-gamma poly
                                                                                                                                                 polype
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Human Gl protein 1
Human FLICE-like 1
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FLICE-like inhibit
Huamn MRIT prodoma
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MRIT-D/S polypept1
Mouse FLIP-c prote
  Human apoptosis as
                                                                                                                                          MRIT-Bam polypepti
MRIT beta 2 polype
                                                                                                                                                                                                 Human MRITalpha
                                                                                                                                                                                                                                                                                                                 Gl protein; CASH-alpha; human; caspase homologue; Fas receptor; modulator; apoptosis; cell death; inflammation; tumour; HIV;
                                                                                                                                                                                                                                                                                                                                                             2..73
/note- "death domain/MORT module"
                                                                                                                                                                                                                                                                                                                                                                              /note= "death domain/MORT module"
                                                                                                                                                                                                                                                                                                      Human G1 protein isoform alpha (CASH-alpha).
                                                                                                                                                                                                                                    ALIGNMENTS
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AAX05790
AAX05793
AAX05793
AAX05793
AAX05795
AAX7459
AAX7465
AAX7465
AAX03794
AAX03794
AAX05794
AAX05794
AAX05794
AAX05794
                        AAY59414
AAW90107
AAX501007
AAX67419
AAX67419
AAX021591
AAX05791
AAX05792
AAW69230
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AAW69230
AAW69230
                  AAW76625
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                  AAW78903 standard; Protein; 480 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              97IL-0120759.
97IL-0120367.
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01-MAY-1997;
03-MAR-1997;
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2435.5
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2265.5
2265.5
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VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP

361

Varfolomeev

Mon Aug

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This is the amino acid sequence of the alpha isoform of novel human G1 protein. The sequence is deduced from an isolated skin cc human G1 protein. The sequence is deduced from an isolated skin cf libroblast cDNA clone (see AAV52968). G1-alpha (also called CASH alpha, CASH being caspase homologue) and a shorter isoform, G1-beta (see AAW7804), represent 2 splice variants of the G1 protein. These CG is proteins are capable of binding to, or interacting directly or indirectly, via their N-terminal MORT modules, with MORT-1 or with MORT-binding proteins such as Much (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular domain of the FAS-R such as a mediators or of binding to the intracellular commain of the p55 tumour necrosis factor (TANP) receptor, to which MORT-1 binds, or of binding of the intracellular commain of the p55 tumour necrosis factor (TANP) receptor, they care considered as mediators or modulators of FAS-R having a role in CG or, the signalling process that is initiated by the binding of TANF to P55-R. The longer isoform also case used to requiate call death or inflammatory processes. (II) is care used to requiate call death or inflammatory processes. (II) is care used to requiate call death or inflammatory processes. (II) is coll death, and its inhibitors augment/enhance the processes. (I) and (II) requiate the FAS-R ligand or TWF effect on the sequence encoding (II), which kills the cell. Antisense cells can be treated using a viral vector encoding a viral suffaces protein, which binds a specific cell surface receptor and a cellects can also be regulated using a vector encoding a ribozyme celects can also be regulated using a vector encoding a ribozyme celects.
                                                                                                                                                                 New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate the effects of FAS and tumour necrosis factor receptors, useful for killing of cells e.g. HIV and cancer cells
                         Kovalenko A,
                                                                                                                                                                                                                                                                     Claim 12; Fig 1B; 132pp; English
                       Brodianski V, Goltsev Y,
                                                                                               WPI; 1998-495842/42.
                                                                                                                        N-PSDB; AAV52968.
                                                   Wallach D;
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480 AA; Sequence

ö 120 180 240 240 300 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFIMKDYM 120 180 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360 9 9 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILKERGKLSVGDLAELLY

1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILKERGKLSVGDLAELLY SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP **EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP** Gaps ö 100.0%; Score 2473; DB 19; Length 480; 100.0%; Pred. No. 4.8e-217; ive 0; Mismatches 0; Indels 0; 3est_Local Similarity 100.
4atches 480; Conservative 121 241 61 181 181 241 Query Match 61 301 301 ò g ö 9 Q ò 요 õ 윱 à à g

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361 VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHRRADFFWSLCTADMSLLEQSHSSP 420
                                    SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYWWLQHTLRKKLILSYT 480
                                                  RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFILMKDYM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP
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                                                                                                                                                                                                                          Death effector domain; human; murine; anti-apoptotic; treatment; HIV infection; autoimmune disease; FLIP protein.
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P, Schroeter M, Steiner V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 480;
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99.8%; Pred. No. 1.4e-216;
ive 1; Mismatches 0;
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, Schneider F
Hofmann K;
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Matches 479; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       (TSCH/) TSCHOPP J. (APOT-) APOTECH SA.
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Irmler M,
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I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease; CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis; CNS inflammation; osteoporosis; ischemenia; polycystic kidney disease; multiple sclerosis; head injury; cancer; autoimmune disorder; therapy; viral infection; graft versus host disease; graft rejection.
                                                                                                     RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM
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970S-0034205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a novel human protein, designated Casper (for caspase-eight-related protein), that is involuted in regulation of apoptosis. The sequence is deduced from an isolated cDNA clone (see AAV50436). Casper protein interacts with FADD and is recruited to Fas. It also interacts with caspase-8 and caspase-3, and with TRAFI and TRAF2. A claimed isolated polypeptide comprises the full-length Casper amino acid sequence, or a fragment of at least 6 consecutive amino acid residues including at least one of residues 1-96, 1-202, 1-435, 78-480, 192-480, 390-480 or residue 80. The isolated protein, or cells that express the protein, can be used to screen for agents, e.g. antibodies or T-cell receptors, that specifically modify the binding of Casper to a target, and thus its function.
                                                                                                                                                                                                                     EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP
                                                                                                                   EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
                                                                                                                                                                                                 VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
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Pred. No. 1.4e-216;
1; Mismatches 0;
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N-PSDB; AAV50436.
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                                                                                                                                                                                                                                  Theumatoid arthritis), and virtal infections (e.g. herpes viruses, pox viruses and adenoviruses), graft versus host disease, acute disease, acute graft rejection, and chronic graft rejection. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the first examples of a naturally occurring catalytically inactive caspase that can act as a dominant negative inhibitor of apoptosis. The oblypeptides and agonists can be used for treating e.g. Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury, cell death associated with cardiovascular disease, polycystic kidney disease, apoptosis of endothelial cells in cardiovascular disease, degenerative liver disease, multiple sclerosis (MS) and head injury damage. Antagonists of the polypeptides can be used for treating cancers (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-dependent tumours, and cancers of the breast, ovary, prostate, bone, liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic lupus erythematosus, immune-related glomerulonephritis,
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                          This sequence is an inhibitor of of Fas-ligand associated with death domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;
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Pred. No. 1.4e-216;
1; Mismatches 0;
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Claim 9; Fig 1; 118pp; English.
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The present sequence represents human FIN-1 (FLICE inhibitor-1), which is a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting enzyme family, a protein involved in the regulation of cell death. A host cell, comprising a vector containing FIN-1 encoding DNA, can be used to produce FIN-1. The vector containing the DNA can be used for producing a cell which expresses a polypeptide by transforming or transfecting the cell with it so that the cell expresses the polypeptide concoded the human cDNA contained in the vector. The polypeptide or its antagonist can be used in the treatment of patients needing FIN-1 by in-vivo administration. Conditions which may be treated include viral infection, tumours (especially solid tumours), ischaemic injury (e.g. stroke or myocardial infarction), neurodegenerative disorders (e.g. Dolycystic kidney disease, chronic degenerative liver disease, acquired immunodeficiency syndrome (AIDS) and applastic anaemia. The polynucleotides may also be used for chromosome identification.
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apoptosis-related protein; caspase; viral infection; cancer; tumour;
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                            diagnosis; ischaemic injury; neuro-degenerative disorder
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Pred. No. 1.4e-216;
1; Mismatches 0;
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N-PSDB; AAV31375.
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181 SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP 240
                                                                                                                                                            SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLILSYT 480
                     EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
                                                                                                                VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
                                                                                                                                                                                                                                                                                                                                                 pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; aplastic anaemia; myocardial infarction; therapy.
                                                                                                                                                                                                                                                                                                                                      MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "death effector domain homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identifying regulators of MACH-related inducer of toxicity
                                                                                                                                                                                                                                                                                                               Human MACH related inducer of toxicity MRIT alpha 1.
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/note= "caspase homology region"
358..362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human FLICE-like inhibitory protein long form, designated FLIP-L. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FID molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and
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                                                                                                                                                                                                                             FLICE-like inhibitory protein short form; apoptosis inhibitor; arteriosclerosis; vascular wall inflammation; vascular injury; Fas ligand-mediated apoptosis; atherosclerosis; transplant.
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                                                                                                                                                                                            Human FLICE-like inhibitory protein long form protein sequence
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The present sequence represents novel human MACH-related inducer of toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that interacts simultaneously with caspases and Bcl-2 family be polypeptides, and which has pro-apoptotic activity. Multiple soforms of MRIT have been identified, some of which function to induce caspase dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AX105789), while others have anti-apoptotic activity, e.g. MRIT alpha 2 (see AX105788). MRIT alpha 1 includes an N terminal death effector domain and a c-terminal caspase homology domain, but is not a cysteine protease. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation. A cell accumulation disorder such as cancer, autoimmune disease, viral infection,
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                                                                                                                                                                                                                                       angiogenesis or atherosclerosis is treated by administering an agent that selectively enhances MRIT apoptotic activity, thereby inducing apoptosis in a subject. A disorder of cell loss, such as a neurodegenerative disorder, including Alzheimer's disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial infarction or AIDS can be treated by administering an agent that selectively inhibits MRIT apoptotic
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Pred. No. 1.4e-216;
1; Mismatches 0;
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Best Local Similarity 99.8
Matches 479; Conservative
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anti-apoptotic polypeptide which comprises a portion of an anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transporting the chimeric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibiting protein (FLIP) which inhibits Rs and THF mediated apoptosis by inhibiting binding of Caspase-8 to the Fas areceptor complex, thus shutting off the downstream Fas signalling pathway. The chimeric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimeric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing T cells antigens and as tumour-specific antigen, for enhancing T cells antigens and set inhibit the apoptosis of chronically activated chimeric group is also useful for therapeutic, prophylactic or the chimeric group is also useful for therapeutic, prophylactic or macromolecules such as anti-apoptotic polypeptides and nucleic acids encoding such polypeptides.
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apoptosis; caspase-8; ligand; T cell; thymocyte, antigen; immune response; therapy; prophylaxis; human immunodeficiency syndrome; AIDS;
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Pred. No. 1.4e-216;
1; Mismatches 0;
                                                                                                deficiency syndrome; human.
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(ALGE/) ALGECIRAS-SCHMINICH A.
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99.8%;
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99US-0128021.
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479; Conservative
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   FLIP; Fas; TNF;
tumour specific
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06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             usurpin-beta;
immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant DNA molecules and polypeptides for treating apoptosis mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
                                                                                                                                                                                                                                                                              VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
                                                                           EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
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99.8%; Pred. No. 1.4e-216;
11ve 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic; antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator; cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer; immune disorder; rheumatoid arthritis; systemic lupus erythematosus; reproductive disorder; tumour; gastrointestinal disorder; cirrhosis; colitis; hepatitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or preventing disorders associated
                                                                                                     SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP
                                                                                                                                                                                    EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP
                                                                                                                                                                                                 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
                                                                                                                                                                                                                                             VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler KJ, Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human apoptosis associated protein HAPOP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein for diagnosing, treating of with increased or decreased apoptosis
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Dean NM;

Ricketts W,

Watt AT,

Zhang H,

Ackermann EJ, Bennett CF,

2002-401983/43.

N-PSDB; ABL52333

(ISIS-) ISIS PHARM INC

14-SEP-2001; 2001WO-US28732

WO200224717-A1 Homo sapiens.

tumour.

28-MAR-2002

2000US-0666269

20-SEP-2000;

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The present sequence represents a human apoptosis associated protein designated HAPOP-1. HAPOP proteins are apoptosis regulators which have antiarteriosclerotic, cytostatic, antiarthritic and hapatotropic activity. A pharmaceutical composition compurising HAPOP in conjunction with a carrier, a purified antagonist of HAPOP, vectors and agonists of HAPOP, are administered for diagnosing, treating or preventing disorders associated with increased or decreased apoptosis, e.g. cell proliferative disorders such as atherosclerosis, arteriosclerosis and cancers; immune disorders such as rheumatoid arthritis, systemic lupus erythematosus; creproductive disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as prostate cancer, endometrial and ovarian tumours; and gastrointestinal disorders such as prostate cancer, and or the orrelated with diseases and are also useful to detect differences in the chromosomal location due to translocation, inversion etc., among normal, carrier, or affected individuals. The combination of the therapeutic agents may act synergistically to effect the treatment or prevention of various disorders providing improved efficacy with lower designed and thus reducing the potential for adverse side
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anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
phosphorothioate; antisense modulation; infection; inflammation;
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Pred. No. 1.4e-216;
1; Mismatches 0;
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Matches 479; Conservative
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The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule (II) encoding a natural dominant negative regulator of caspase 8, Filp-C, where (I) specifically of pridises with and inhibits expression of the protein of an active site on hybridises with at least an 8-nucleobase portion of an active site on (II). (I) has antinflammatory and anti-tumour activities. (I) is an inhibitor of Filp-C expression, a modulator of apoptosis and can be used inhibitor of Filp-C expression, a modulator of apoptosis and can be used of Filp-C in cells or tissues, and for treating an animal having a disease or condition associated with Filp-C. (I) is also useful for modulating apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or caspase 7 is activated, and the Filp-C is the long form of Filp-C. (I) is also useful for diagnostics, therapeutics, prophylaxis, as research caspase and in antisense gene therapy. (I) is also useful compophylactically, e.g., to prevent or delay infection, inflammation or the present invaries represents human Filp-C as given in a caspase in a caspase or complylactically.
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                                                                                                                                                                                                                                                                                                                                   Novel antisense compound that hybridizes and inhibits nucleic acid encoding a natural dominant negative regulator of caspase 8, FLIP-c, useful for preventing or delaying infection, inflammation or tumor
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99.8%; Pred. No. 1.4e-216;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 118-120; 154pp; English.
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Matches 479; Conservative
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                                                                                                         12 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Death effector domain; human; murine; anti-apoptotic; treatment; HIV infection; autoimmune disease; FLIP protein.
                                  Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FLIP protein fragment containing death effector domain.
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P, Schroeter M, Steiner
                                                              Indels
                                DB 21;
                               Score 2468; DB 21;
Pred. No. 1.4e-216;
                                                           1; Mismatches
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, Schneider F
Hofmann K;
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                               99.8%;
99.8%;
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                                                              Conservative
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Irmler M, Rimoldi D,
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                               Query Match
Best Local Similarity
Matches 479; Conserv
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   491 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-apoptotic polypeptide which comprises a portion of an anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transporting the chimaric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits Ras and TWIR mediated apoptosis by inhibiting binding of Caspase-8 to the Fas receptor complex, thus shutting off the downstream Fas signalling pathway. The chimaric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimeric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing T cells antigens and as tumour-specific antigen, for enhancing T cells e.g. activated CD4** T cells in MIV infected patients. The chimeric group is also useful for therapeutic, prophylactic or macromolecules such as anti-apoptotic polypeptides and nucleic acids encoding such as anti-apoptotic polypeptides and nucleic
                                                                                       480
                                                                                                      301 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIONY 360
                                             VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
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                                                                                                                                                                                                                                                                                                              Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte; tumour specific antigen; immune response; therapy; prophylaxis; diagnosis; HIV; human immunodeficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                            diagnosis; HIV; human immunodeficiency synd acquired immune deficiency syndrome; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 84-85; 89pp; English.
                                                                                                                                                                                          AAB03964 standard; Protein; 491 AA.
                                                                                                                                                                                                                                                                                 FLIP with detectable peptide tag.
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(ALGE/) ALGECIRAS-SCHMINICH A.
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99US-0128021
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Synthetic.
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                              Nunez G,
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                            This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and autoimmune diseases.
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                                                                                                                                                                                                                                  SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP
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                                                                                                                                                                                                                                                                                                                  1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                    GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
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                                                                                                                                                                                                                                                                                                                                                                                       VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
                                                                                                                       Gaps
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                                                                                                                      1;
                                                                                                    DB 19; Length 479;
                                                                                                  Score 2435.5; DB 19; Lengt
Pred. No. 1.3e-213;
1; Mismatches 3; Indels
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          German
                                                                                                   98.5%;
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                                                                                                            Best_Local Similarity 99.03
Matches 475; Conservative
         Fig 3; 45pp;
                                                                                479 AA;
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         Disclosure;
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This sequence is the human CLARP protein. The invention relates to the human RICK (RIP-like interacting CLARP kinase) protein. The RICK the human RICK (RIP-like interacting CLARP kinase) protein acts as a positive regulator of apoptosis, protentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions, compositions of the various compositions, and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and county and yastegulation of apoptosis. Complexes containing RICK and molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds and be used to treat e.g. cancer, ALDS, neurodegenerative compositions of disoaces and in muscle tissue and cardiac disoaders. ALDS, neurodegenerative disoaces and cardiac disoaders. ALDS, neurodegenerative disoaces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the blochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                    Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Fig 21b; 93pp; English.
                                                                                                            Inohara N, · Koseki T;
UNIV MICHIGAN
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apoptotic agents.

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This is the amino acid sequence of human FLAME-1, or FADD-like apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic protein that interacts specifically with FADD, McM4, Mch5 and FLAME-2. It is recruited to the Fas receptor complex and can abrogate Fas/TNF-induced apoptosis upon expression in Fas/TNF-sensitive MCF-7 cells. Despite having a caspase domain-like region, it does not have caspase activity. The amino acid sequence of FLAME-1 was deduced from the nucleotide sequence (see AAV74136) of a Jurkat cell-derived cDNA clone. Host cells, recombinant vectors, and methods of using FLAME-1 to identify substrates, activators or inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see AM99108) and agonists can be used to inhibit apoptosis, e.g. for treating HIV infection or Alzheimer's disease. Inhibitors can be used as
                                                                                                                                                                                                                                                                              1.341
/note= "p39 subunit, specifically claimed in Claim
                                                                                                                                                                                                                                                                                                                         /note="pl2 subunit, specifically claimed in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "caspase cleavage site, generating p39 and p12"
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                                                                                                                                                                                               FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human; apoptosis; HIV; infection; Alzheimer's disease; cancer; therapy,
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apoptotic and anti-apoptotic agents for treating, e.g. HIV
infection, Alzheimer's disease or neoplastic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                          "caspase-domain homology region"
                                                                                                                                                                                                                                                                                                                                                                      "FADD-DED homology A"
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te= "active site motif"
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                                                                                        AAW90107 standard; Protein; 445
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322..32
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197..44
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                                                                                                                                                                     Human FLAME-1 protein.
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                                                                   1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                   Gaps
                                                   35;
                                  DB 20; Length 445;
                                                  Indels
                                Score 2265.5; DB 2
Pred. No. 3.9e-198;
1; Mismatches 0;
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Job time : 84.8531 secs
                               tch 91.6%; sal Similarity 92.5%; 444; Conservative
                445 AA;
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August 13, 2003, 16:43:55; Search time 49.9857 Seconds (without alignments) 1257.990 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_EVBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US0_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2473
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 11, Appl	Sequence 17, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 318, App	Sequence 37, Appl	Sequence 6, Appli	Sequence 12, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 22, Appl	Sequence 36370, A	Sections 20 April
	ID	US-09-861-270-2	US-09-410-194-11	US-09-410-194-17	US-09-009-893-2	US-09-471-749-1	US-10-103-313-318	US-10-115-928-37	US-09-009-893-6	US-09-410-194-12	US-09-410-194-19	US-10-005-921-2	US-09-410-194-15	US-09-410-194-22	US-09-864-761-36370	US-08-410-194-20
	DB	6	σ	σ	11	11	15	15	1	σ	6	14	σ	σ	6	σ
	Query Match Length DB	:						391	348	481	481	484	221	221	93	479
dР	Query Match	8.66	99.8	8.66	8.66	99 B	80.6	90.6	62.9	63.9	63.9	63.4	40.7	40.7	18.8	16.6
	Score	2468	2468	2468	2468	2468	1993	1993	1630	1580	1580	1568.5	1007	1007	465	410
	Result No.	1	7	Э	4	2	9	7	8	6	10	11	12	13	14	15

NAME: Osman, Richard A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: T97-001 TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 480 amino acids

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,088
FILING DATE: <Unknown>
ATTORNEY/AGENT INPRMATION:

Sequence 3, Appli Sequence 35073, A	Sequence 4, Appli Sequence 27, Appl	Sequence 2, Appli	7		Sequence 33, Appl	Sequence 4, Appl1	ñ	H	4	Sequence 2, Appl1	23	Sequence 48, Appl	4	5,	\sim	Sequence 5, Appli	Sequence 48728, A	Sequence 7, Appli	_		Sequence 202, App		m	12,	Sequence 36, Appl	Sequence 52, Appl	28,
11 US-09-009-893-3 9 US-09-864-761-35073	9 US-09-952-768-4 10 US-09-954-697-27	9 US-09-962-834A-2	9 US-09-410-194-21	9 US-09-952-768-2	10 US-09-954-697-33	11 US-09-009-893-4	9 US-09-410-194-24	9 US-09-862-915-1	9 US-09-410-194-4	9 US-09-410-194-2	9 US-09-410-194-23	10 US-09-989-903-48	15 US-10-068-564-48	9 US-09-410-194-5	10 US-09-954-697-21	15 US-10-171-077-5	9 US-09-864-761-48728	9 US-09-410-194-7	9 US-09-895-263-4	15 US-10-214-932-108	15 US-10-207-655-202	14 US-10-103-448-3	14 US-10-108-929-3	10 US-09-954-697-12	10 US-09-954-697-36	12 US-10-205-219-52	10 US-09-888-243-28
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16.5	15.4	13.1	13.1	12.9	12.9	12.9	10.0	10.0	9.7	9.5	9.5	8.2	8.5	8.0	7.8	7.8	7.7	7.5	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.2	7.2
408.5	381.5	323,5	323.5	318.5	318.5	318.5	248	246.5	239	234	234	204	204	198.5	192	192	191.5	185.5	184	184	184	181	181	181	180	177.5	177
16	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ESULT 1 S-09-861-270-2 Sequence 2, Application US/09861270 Sequence 3, Application US/09861270 Sequence 3, Application US/09861270 TITLE OF INVENTION: Regulators of Apoptosis NUMBER OF SCUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSES: Science 5 Technology Law Group STREET: 75 Denise Drive CITY: Hillsborough STATE: California COUNTRY: USA ZIP: 94010 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBW PC COMPATA: MEDIUM TYPE: Ploppy disk COMPUTER: IBW PC COMPATA: MEDIUM TYPE: Patentin Release #1.0, Version #1.30 RILING DATE: 18-MAY-2001 FILING DATE: 18-MAY-2001 FILING DATE: 18-MAY-2001 CLASSIFICATION: CURNOWN>

ALIGNMENTS

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Homo sapiens
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                                                                                            Length 480
                                                                                                                   Indels
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APPLICANT: Schrotter, Michael
APPLICANT: Schrotter, Michael
APPLICANT: Schrotter, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: French, E. Lars
APPLICANT: REPERENCE: 11141-002001
                                                                                      Score 2468; DB 9;
Pred. No. 1.4e-218;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCI/EP98/01857
PRIOR FLIKW DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
STRANDEDNESS: not relevant
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/410,194 CURRENT FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-410-194-11
; Sequence 11, Application US/09410194
; Setter No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
                                                                                         99.8%;
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Burns, Kimberly
                                                                                          Query Match 99.8
Best Local Similarity 99.8
Matches 479; Conservative
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                                             Gaps
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Length 480;
                                          Indels
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APPLICANT: Schroider, Pascal
APPLICANT: Schroider, Pascal
APPLICANT: Schroider, Pascal
APPLICANT: Steiner, Veronique
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFRERENCE: 11141-00200,
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT APPLICATION NUMBER: PCT/EP98/01857
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1997-04-01
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Score 2468; DB 9;
Pred. No. 1.4e-218;
1; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 480
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99.8%;
99.8%;
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APPLICANT: Burns, Kimberly
APPLICANT: Irmler, Marten
APPLICANT: Hahne, Michael
                       Best_Local Similarity 99.8
Matches 479; Conservative
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US-09-410-194-17
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301 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360
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Sequence 1, Application US/09471749

Sequence 1, Application No. US20030124113A1

GENERAL INFORMATION:

APPLICANT: Hilman, Jennifer L.

APPLICANT: Gorley, Nell C.

APPLICANT: Baughn, Mariah

TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

STREET: ALO ALC

STREET: SALO
                                                                                                                                                                                                                         Length 480;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                        Score 2468; DB 11;
Pred. No. 1.4e-218;
1; Mismatches 0;
         NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
                                                                                                                                                                                                                        99.8%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.8<sup>1</sup>
Matches 479; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-009-893-2
                                                                                                                                                                 linear
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APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR.
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS CORRESPONDENCE ADDRESS:
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                                                                                      1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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                                                                    1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                          Gaps
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          Length 480;
                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
          8; DB 9;
1.4e-218;
          Score 2468; I
Pred. No. 1.46
1; Mismatches
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APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/054,800 FILING DATE: 05-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
          99.8%;
99.8%;
                         Best Local Similarity 99.8
Matches 479; Conservative
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          Query Match
Best Local (
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Best Local 3
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Sequence 318, Application US/10103313

Publication No. US20030082758A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ07C1
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                        Score 2468; DB 11;
Pred. No. 1.4e-218;
1; Mismatches 0;
            SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                                                                                   NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0519 US
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/471,749
                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/078,402
                                                                                                                                                                                                                                                                                                                                                                     99.88;
                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.8<sup>1</sup>
Matches 479; Conservative
                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                   LIBRARY: THP1PLB02
CLONE: 157658
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                                                                                                           FILING DATE:
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                                                                                                                                                                             NAME/KEY: misc_feature

1 LOCATION: (97)

2 OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids

US-10-103-313-318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 GYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLH
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CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 318
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or Palm
                                                                                                                                                                                                                                                                               Query Match 80.6%; Score 1993; DB 15; Best Local Similarity 99.5%; Pred. No. 5.6e-175; Matches 384; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10115928
Publication No. US20030092615A1
EMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZQ4C1
CURRENT APPLICATION NUMBER: US/10/115,928
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 74 SOGTWARE: Patentin Ver. 2.0 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 SRVSAKEKYYVWLQHTLRKKLILSYT 480
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ORGANISM: Homo sapiens
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Best Local Similarity
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Matches 384; Conserva
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157 KNIHRIDLKTKIQKYKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQ 216
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66.9%; Pred. No. 8e-137;
ive 56; Mismatches 97; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
                                                                                                                                             Query Match 65.9%; Score 1630; DB 11;
Best Local Similarity 93.8%; Pred. No. 1.2e-141;
Matches 318; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2 PRIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 27 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12 LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
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: Rimoldi, Donata
: Hofmann, Kay
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APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean- Luc
             LENGTH: 348 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-6
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APPLICANT: Burns, Kimberly
APPLICANT: Irmler, Marten
APPLICANT: Hahne, Michael
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Best Local Similarity 66.9
Matches 322; Conservative
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus
US-09-410-194-12
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US-09-410-194-12
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Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: DIXIT, VISHVA M.
APPLICANT: RENER L.
APPLICANT: RENER L.
APPLICANT: RENER L.
APPLICANT: APPLICANT: RENER L.
APPLICANT: OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              EQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRDTFTSL 274
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                                                                                                                                                                                                                                                                                                                                                               HIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCT 394
                                    6 VLMARIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLER
                                                                                                   155 CLKNIHRIDLKTKIQKYKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLK
               95 VLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEK
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CITY: WASHINGTON
STATE: DC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRVSAKEKYYVWLQHTLRKKLILSYT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 SRVSAKEKYYVWLQHTLRKKLILSYT 391
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FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : STEFFE, ERIC K.
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61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFL---MK 117
                                                                                                     GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                                            SYRNVLQAAIQK-SLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSI 239
                                                                                                                                                                                                                                                     240 PEERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACM 299
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                                                                                    RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                                                                                                                                                        1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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             MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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; Sequence 2, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
    APPLICANT: Allen, Keith D.
    TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
    TITLE OF INVENTION: DISRUPTIONS
    FILE REPERENCE: R-7.14
    CURRENT APPLICATION NUMBER: US/10/005,921
    CURRENT FILING DATE: 2000-12-04
    PRIOR FILING DATE: 2000-12-11
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: FRASES for Windows Version 4.0
    SEQ ID NO 2.
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Best Local Similarity 66.5%; Pred. No. 9.2e-136;
Matches 322; Conservative 56; Mismatches 97;
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CRGANISM: Mus musculus
US-10-005-921-2
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                                                                 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                    GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                                                                                                                                                           MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                181 SYRNVLQAAIQK-SLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSI
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APPLICANT: TSCHOOP, JUIGG
APPLICANT: TSCHOOP, Margot
APPLICANT: Irmler, Marten
APPLICANT: Irmler, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schoeider, Pascal
APPLICANT: Schoeider, Pascal
APPLICANT: Steiner, Veronique
APPLICANT: Steiner, Veronique
APPLICANT: Hofmann, Kay
APPLICANT: Hofmann, Kay
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROFEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1998-03-31
PRIOR PILICATION NUMBER: GERMANY 197 13 393.2
PRIOR PILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SSOFTHARE: FASTSEQ for Windows Version 4.0
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66.9%; Pred. No. 8e-137;
ive 56; Mismatches 97;
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Patent No. US20020095030A1
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Best Local Similarity 66.9
Matches 322; Conservative
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Steiner, Veronique
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Best Local Similarity 99.5%;
Matches 202; Conservative
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Schneider, Pascal
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Burns, Kimberly
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Hahne, Michael
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US-09-410-194-22
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QSIPEERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQF
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                                                  AGTSYRNVLQAAIQK-SLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLP
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APPLICANT: Halne, Michael
APPLICANT: Halne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schoelder, Dean-Luc
APPLICANT: Rinchid, Donata
APPLICANT: Rinchid, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
APPLICANT: PRINCH PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: APPLICATION NUMBER: PCT/EP98/10713-303-7
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99.5%; Pred. No. 1.4e-84;
11ve 1; Mismatches 0;
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Patent No. US20020095030A1
GENERAL INFORMATION:
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Burns, Kimberly
Irmler, Marten
Hahne, Michael
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Matches 202; Conservative
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LAPT 484
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LENGTH: 221
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
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121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
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APPLICANT: French, E. Lare
TILLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR PPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1999-04-01
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Pred. No. 1.4e-84;
1; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 221
                                                                         Sequence 36370, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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215 --QIL-DKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAG 268
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4.1e-29;
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TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                  Sequence 20, Application US/09410194 Patent No. US20020095030A1
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Schneider, Pascal
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Hahne, Michael
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Best Local Similarity
Matches 137; Conserv
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SWISSPROT HIT: Q66674, EVALUE 3.00e-04
EST_HUMAN HIT: W23795.1, EVALUE 2.00e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIN LUNG, SIGNAL = 8

ED IN BRAIN, SIGNAL = 2

ED IN PLACENTA, SIGNAL = 1.9

ED IN HELLOO, SIGNAL = 1.9

ED IN HELLO, SIGNAL = 3.3

ED IN BT474, SIGNAL = 3.6

ED IN BT474, SIGNAL = 2.6

ED IN BT474, SIGNAL = 2.5

ED IN ADULT LIVER, SIGNAL = 2

ED IN ADULT LIVER, SIGNAL = 2

FILT: 066674, EVALUE 3.00e-04
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN BONE MARROW, SIGNAL = 2.5
EXPRESSED IN LUNG, SIGNAL = 8
                                                                                                  CURKENT FILLING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30

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Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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US-09-864-761-36370
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Indels 110; Length 479;

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 13, 2003, 16:33:14 ; Search time 20.5421 Seconds (without alignments) 1098.857 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-380-546A-2
2473
1 MSAEVIHQVEEALDFDEKEM......EKYYVWLQHTLRKKLILSYT 480

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

å Query Score Match Length DB ID
1
.4 484 1
17.0
16.6
y L
5 7.7 282 1
7.7
7.6
7.3
7.3
7.2
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9 10
152 6.1 323 1
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5 5.8
2 5.7
.5 5.6
5 5.4
.5 5.4
4.
5.3 4
129 5.2 404 1

P70343 mus musculu P29466 homo sapien 014248 schizosacch Q8wxh0 homo sapien P29452 mus musculu P42573 caenorhabdi 007970 arabidopsis P58301 pyrococcus 014573 homo sapien 063269 rattus norv 075601 bos taurus 014157 schizosacch
ICEB_MOUSE IIBC_HUMAN STEG_SCHPO SNEZ_HUMAN IIBC_MOUSE CED3_CAEEL RASO_PYRFU IP3T_RAT ICED_BOYIN MYS3_SCHPO
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373 404 1125 6885 6885 703 793 882 2671 2670 377
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126.5 126.5 126.126.126.5 125.5 121.5 121.5 121.121.121.121.121.121.120.1116.5
33 33 33 33 34 44 44 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37

## ALIGNMENTS

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TESSUE-Lymph,

WEDLINE-22388257; PubMed-12477932;

WEDLINE-22388257; PubMed-12477932;

MELAUSERE-Lymph,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wanger L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Chards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Villalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shèvchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Lenner A. Schein J.E., Jones S.J.M., Marra M.A.;

R. "Lenner A. Schein J.E., Jones S.J.M., Marra M.A.;

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R. "Lenner A. Schein J.E., Diones S.J.M., Marra M.A.;

R. "Lenner A. Schein J.E., Jones S.J.M., Marra M.A.;

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R. "Lenner A. Schein J.E., Diones S.J.M., Marra M.A.;

R. "Lenner A. Schein J. "Lenner A. Schein J. "Lenner A. "
                                                                                                                                                                                                                                                                               Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I., Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D., Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P., Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S., Nicholson D.W.; Micholson D.W.; Roy S., Cell death attenuation by 'Usurpin', a mammalian DED-raspase
                                                         Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.; "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inohara N., Koseki T., Hu Y., Chen S., Nunez G., "CLARP, a death effector domain-containing protein interacts with
                                                                                                                                                                                                                                                                                                                                                                                 "Cell death attenuation by 'Usurpin', a mammalian DED-caspase homologue that precludes caspase-8 recruitment and activation by CD-95 (Ras, APO-1) receptor complex."; Cell Death Differ. 5:271-288(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CASH, a novel caspase homologue with death effector domains."; J. Biol. Chem. 272:19641-19644(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99098897; PubMed-9889531; Scaffidi C., Schmitz I., Krammer P.H., Peter M.E.; "The role of c-FLIP in modulation of CD95-induced apoptosis."; J. Biol. Chem. 274:1541-1548(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
Brodianskii V.M., Wallach D.;
                                                                                                                                                                          Hu S., Dixit V.M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspase-8 and regulates apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Umbilical vein endothelial cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                               CD-95-induced apoptosis.";
J. Biol. Chem. 272:17255-17257(1997).
                                                                                                                                                                                                                                                  TISSUE-Kidney;
MEDLINE-99218584; PubMed-10200473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Colon carcinoma;
MEDLINE-98021435; PubMed-9380701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Skin fibroblast;
MEDLINE-97426025; PubMed-9289491;
                                         MEDLINE-97362203; PubMed-9211860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). BCL-X(L) (IN VITRO).

-I-ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=14;
Name=1; Synonyms=Filp-L, ClarRP, MRIT alpha-1, CASH alpha, I-FLICE
1, FLAME-1 gamma, Usurpin alpha;
IsoId=015519-1; Sequence=Displayed;
Name=2; Synonyms=Filp-S, ClarRP2, MRIT beta-1, CASH beta;
IsoId=015519-2; Sequence=VSP_000828, VSP_000829;
Name=3; Synonyms=MRIT alpha-2;
IsoId=015519-3; Sequence=VSP_000824, VSP_000838;
Name=4: Synonyms=I-FLICE 2;
IsoId=015519-4; Sequence=VSP_000825;
Name=4: Synonyms=I-FLICE 3;
Name=4: Synonyms=I-FLICE 3; TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN
STELETAL MÜGGLE, PANCREAS, HEARY, KIDNEY, PLACENTA, AND PERIPHERAL
BLOOD LEUKCCYTES, ALSO DETECTED IN DIVERSE CELL LINES. ISOFORM 8
IS PREDOMINANTLY EXPRESSED IN TESTIS AND SKELETAL MUSCLE.
INDUCTION: REPRESSED BY IL-2 AFFER TOR STIMULATION, DURING
PROGRESSION TO THE S-PHASE OF THE CELL CYCLE.
DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES FASTMEDIATED TO THE TOTAL THE CONTROL OF THE CONTRO APOPTOSIS OR TO REDUCE THERSE-TRIGGERED APOPTOSIS. LACKS ENZYMATIC (CASPASE) ACTIVITY. SUBUNIT: THERSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-INDUCING SIGNALING COMPLEX (DISC) FORMED BY THERSF6, FADD AND CASPASE-B. A PROTECLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE DISC. ALSO INTERACTS WITH CASPASE-10, CASPASE-3, TRAF1, TRAF2 AND BCL-X(L) (IN VITRO). INVOLVED IN CATALYSIS.
--- PTM: PROTEOLYTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
--- SIMILARITY: Contains 2 death effector (DED) domains. Algeciras-Schimnich A., Griffith T.S., Lynch D.H., Paya C.V.; "Cell cycle-dependent regulation of Filp levels and susceptibility to Name=8; Synonyms-Flame-1 alpha; IsoId=015519-8; Sequence-VSP_000830; Name=9; Synonyms-Flame-1 beta; IsoId=015519-9; Sequence-VSP_000830, VSP_000836, VSP_000837; Name=10; Synonyms-Flame-1 delta; VSP_000827, VSP_000838; IsoId=015519-12; Sequence-VSP_000832, VSP_000833; Isoid=015519-5; Sequence-VSP_000840; Name=6; Synonyms=I-FILCE 4; Isoid=015519-6; Sequence-VSP_000826, VSP_000841; Name=7; Synonyms=I-FILCE 5; Isoid=015519-7; Sequence-VSP_000824, VSP_000827, IsoId=015519-10; Sequence=VSP_000834, VSP_000835; Name=11; Synonyms-Usurpin beta; IsoId=015519-11; Sequence=vSP_000838; Name=12; Synonyms-Usurpin gamma; IsoId=015519-13; Sequence=VSP_000831; IsoId=015519-14; Sequence=VSP_000839; EMBL; AF010127; AAB64110.1; -. Name-14 Name=13

EMBL; U85059; AAB82648.1; -. EMBL; U97074; AAC51622.1; -.

[12] INDUCTION. MEDLINE-99244884; PubMed-10227994;

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                                                                                                                                                                                                   EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300
                                                                                                                                                                                                                                                             360
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O35722; O35707; O35733;

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-OCT-2001 (Rel. 40, CreIP) (Caspase-eight-related protein) (Caspase-like apoptosis regulatory protein) (Caspase-like apoptosis regulatory protein) (ClaNP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of PLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
CFLAR OR CASH.
                                                                                                                                                                                                                                                                               GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
                                                                                                                                                                       GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
                                                                                                                                                              SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP
                                                                                                                                                                                                                                         EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
                                            MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E., Brodianskii V.M., Wallach D.;
"CASH, a novel caspase homologue with death effector domains.";
J. Biol. Chem. 272:19641-19644(1997).
                           ö
         Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97360133; PubMed-9217161;
Irmler M., Thome M., Hahne M., Schneider P., Hofmann K., St
Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi
French L.E., Tschopp J.;
"Inhibition of death receptor signals by cellular FLIP.";
Nature 388:190-195(1997).
                           Indels
      Score 2468; DB 1;
Pred. No. 7.5e-146;
L: Mismatches 0;
                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
       99.8%;
               Best Local Similarity 99.8
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event—Alternative splicing; Named isoforms=2;

Name=1; Synonyms=FilP-L, CASH alpha;
IsoId=035732-1; Sequence—Displayed;
Name=2; Synonyms=FilP-L, CASH alpha;
IsoId=035732-2; Sequence=vSP_000842, vSP_000843;
InoId=035732-2; Sequence=vSP_000842, vSP_000842, vS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CASPASE-8. PROCESSING
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SWART; SM00031; DED; 2.
PROSITE; PS50168; CASPASE_P20; 1.
PROSITE; PS50168; DED; 2.
Apoptosis; Repeat; Alternative splicing.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20069388; PubMed-10602037; Wang J., Lobito A., Shen F., Hornung F., Winoto A., Lenardo M.J.; Winhibition of Fas-mediated apoptosis by the B cell antigen receptor through C-FLIP.";
MEDLINE-20350661; PubMed-10894163;
Yeh W.-C., Itie A., Elia A.J., Ng M., Shu H.-B., Wakeham A. Mirtsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
Requirement for Casper (c-FLIP) in regulation of death receptor-induced apoptosis and embryonic development.";
Immunity 12:633-642(2000).
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-i- SIMILARITY: Contains 2 death effector (DED) domains.
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Pfam; PF01335; DED; 2.
Pfam; PF00656; Peptidase_C14; 1.
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ALTERNATIVE PRODUCTS:
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                                                                                                                                                                               Gaps
CASP8 AND FADD-LIKE APOPTOSIS REGULATOR SUBUNIT P12 (BY SIMILARITY).
                                                      POLY-SER.
LQNGRSKEPRF -> VSLEPVYGVPA (in 1soform
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                              6
                                                                                                                                                      63.4%; Score 1568.5; DB 1; Length 484; 66.5%; Pred. No. 3.8e-90; ive 56; Mismatches 97; Indels 9;
                                                                                                Missing (in isoform 2).
/FIId=VSP_000843.
MISSING (IN REF. 2).
0BF7A92CB09F5FIF CRC64;
                                                                                      /FIId-VSP_000842
Missing (in isofo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-FEP-2003 (Rel. 42, Last annotation update)
Caspase-8 precursor (EC 3.4.22.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98316661; PubMed-9654089;
Sakamaki K., Tsukumo S.-I., Yonehara S.;
                                             CASPASE.
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484 AA; 55245 MW;
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089110; 035669;
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                                                                                                                       CONFLICT
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REDUINE-22388257; PubMed-12477932;

REDUINE-22388257; PubMed-12477932;

RA Strausberg R.L., Feligodd E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsteh F.,

RA Diatchenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Raha S.A., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Rahay J., Helton E., Ketteman M.J., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schelin J.E., Jones S.J.M., Maria M.A.,

RA Schneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protectlytic fragments of the W-terminal properties (termed CAP3, CAP5 and CAP6) are likely retained in the DISC. Cleaves and activates CASP3, CASP4, CASP7, CASP9 and CASP10. May participate in the GZMB apoptotic pathways. Cleaves ADPRT. Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-I-AMC. Likely target for the cowpox virus CRWA death inhibitory protein. ENRYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
SUBUNIT: Heterodimer of a 18 kba (P18) and a 10 kba (P10) subunit. Interacts with FADD and CFLAR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Highest expression in spleen, thymus, lung, liver and kidney. Lower expression in heart, brain, testis and skeletal muscle. DEVELOPMENTAL STAGE: In the embryo, highest expression occurs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         death-Inducing signaling complex (DISC), whereas additional processing is likely due to the autocatalytic activity of the activated process. GzMB and CASP10 can be involved in these processing events (By similarity).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: Contains 2 death effector (DED) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of the subunits requires association with the
                                                                                   MEDLINE-99057979; PubMed-9837723;
Van de Craen M., Van Loo G., Declercq W., Schotte P.,
van den Brande I., Mandruzzato S., van der Bruggen P., Flers W.,
"Molecular cloning and characterization of mouse caspase-8.";
                                                                                                                                                                 "Molecular cloning and identification of murine caspase-8."; J. Mol. Biol. 284:1017-1026(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                              AND CHARACTERIZATION.
                 Eur. J. Biochem. 253:399-405(1998).
                                                                                                                                                  Vandenabeele P.
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388 SSSHKNY------IPDEADFLLGMATVKNCVSYRDPVNGTWYIQSLCQSLR-ERC 435
    266 LLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVD 325
                                                 271 ALSKTFKELHFEIVSYDDCTANEIHEILEGYQ-SADHKNKDCFICCILSHGDKGVVYGTD 329
                                                                                                   326 QTHSGLPLHHIRRAFMGDSCPYLAGKPKMFFIQ----NY---VVSEGQLENSS-LLEVD 376
                                                                                                                              GREAS--IYDLTSYFTGSKCPSLSGKPKIFFIQACQGSNFQKGVPDEAGFEQQNHTLEVD 387
                                                                                                                                                                                               377 GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERK 436
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MEDILINE-96279827; PubMed-8681377;
Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
Krammer P.H., Peter M.E., Dixit V.M.;
"FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
to the CD95 (Fas/APO-1) death-inducing signaling complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Caspasse-8 precursor (EC 3.4.22..) (ICE-like apoptotic protease 5)
(MORTI-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic protease MCH-5) (CAPSP8 OR MCH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q14790; O14676; Q14791; Q14792; Q14794; Q14795; Q14796; Q15780; Q15806; Q8TDI1; Q8TDI2; Q8TDI3; Q8TDI4; Q8TDI5; Q96T22; Q95C0K4; Q9UQ81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains."; Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
TISSUE-B-cell, and Thymus;
MEDLINE-96279826; Pubbled-8681376;
Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
"Involvement of MACH, a novel MORTI/FADD-interacting protease, Fas/APO-1- and TNF receptor-induced cell death.";
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SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-97373543; PubMed-9228018;
Srinivasula S.M., Ahmad M., Ottille S., Bullrich F., Banks S.,
Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
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                                                                                                                                                                                                                                                                                           437 RPLLDLHIELNGYMYDWNSRVSAKEKYYWWLQ--HTLRKKL 475
                                                                                                                                                                                                                                                                                                                        MEDLINE-96353838; PubMed-8755496;
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DNAQIS -> RQCPRFL (IN REF. 4).

A -> V (IN REF. 2).

VMLFR -> SCSFR (IN REF. 4).

K -> N (IN REF. 4).

W; 045268AE3DE5ED4F CRC64;
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CASPASE-8 SUBUNIT P10.
BY SIMILARITY.
DED 1.
DED 2.
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CASPASE-8 SUBUNIT P18.
BY SIMILARITY
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GO; GO:0005737; C:Cytoplasm; IDA.

GO; GO:0005737; C:Cytoplasm; IDA.

GO; GO:0005015; F:caspase-8 activity; IDA.

GO; GO:0006915; P:apoptosis; IDA.

InterPro; IPR00139; ICE.

InterPro; IPR00139; ICE.

InterPro; IPR001309; ICE.

InterPro; IPR001309; ICE.

InterPro; IPR001309; ICE.

Pfam; PF001315; DED; 2.

Pfam; PF001315; DED; 2.

PRNTT; SM00115; CASPASE_C14; 1.

SMART; SM00115; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; 1.

PROSITE; PS50209; CASPASE_PIO; 1.
                                     EMBL; AP067835; AAC40132.1; JOINED. EMBL; AP067835; AAC40132.1; JOINED. EMBL; AP067839; AAC40132.1; JOINED. EMBL; AP067839; AAC40132.1; JOINED. EMBL; AP067839; AAC40132.1; JOINED. EMBL; AP067840; AAC40132.1; JOINED. EMBL; AJ007749; CAAO40131.1; EMBL; AJ000749; CAAO40131.1; EMBL; AJ000641; CAAO4196.1;
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                        AF067841; AAC40132.1;
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MEROPS; C14.
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MEDLINE-22388257; PubMed-12477932;

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PARTANT CASPBD TRP-248.

RA WENDINE-2239940; PubMed-12353035;

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Caspases responsible for the TWRSP6/FAS mediated and TWRSP6/IA moduced cell death. Binding to the adapter molecule FADD recruits it to either receptor. The resulting aggrapate called death-induced complex (DISC) performs CASPB proteclytic fragments (DISC) performs CASPB proteclytic fragments of the N-terminal propeptide (termed CAP) activate downstream apoptotic proteases.

Cativation. The activate downstream apoptotic proteases.

Proteclytic fragments of the N-terminal propeptide (termed CAPS) activates CASPB, CASPP, CASP Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W., Cromlish J.A., Shore G.C.; "p28 Bap21, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the endoplasmic reticulum."; MEDLINE-99451259; PubMed-10508784; Blanchard H., Kodandapan L., Mittl P.R.E., Di Marco S., Krebs J.F., Wu J.C., Tomaselli K.J., Gruetter M.G.; Tomaselli K.J., Structter M.G.; The three-dimensional structure of caspase-8: an initiator enzyme in "Dominant expression of a novel splice variant of caspase-8 in human peripheral blood lymphocytes."; Biochem. Biophys. Res. Commun. 272:877-881(2000). CHARACTERIZATION OF ISOFORM 7. MEDLINE-20318377; PubMed-10860845; Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C., MEDLINE-97327557; PubMed-9184224; Medema 7.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M., Krammer P.H., Peter M.E.; Resoner P.H., Peter M.E.; Resociation with the CD95 death-inducing VSP_000815; IsoId=Q14790-6; Sequence=VSP_000811, VSP_000812; Event-Alternative splicing; Named isoforms=9; Name=4; Synonyms=Alpha-4; IsoId=Q14790-4; Sequence=VSP_000809, Name-1; Synonyms-Alpha-1; IsoId-014790-1; Sequence-Displayed; Name-2; Synonyms-Alpha-2, MCH5-beta; IsoId-014790-2; Sequence-VSP_000810; IsoId=Q14790-5; Sequence=VSP_000814, IsoId=Q14790-3; Sequence=VSP_000813; INTERACTION WITH BCL2; BCL2L1 AND BCAP31. MEDLINE-97477382; PubMed-9334338; X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). Cell Biol. 139;327-338(1997). Name=3; Synonyms-Alpha-3; Name=5; Synonyms=Beta-1; Structure 7:1125-1133(1999). Name=6; Synonyms=Beta-2; signaling complex (DISC)."; EMBO J. 16:2794-2804(1997). MEDLINE=97477382; Hayashi K.; apoptosis." [15] 

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114 FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQ 173
                                                                                                                                                                                                                                                SIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIG------NETEL--- 266
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                                                                                                    57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI
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                                                                                                                                                                                                                                                                                                                                                                                          -GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE-
                                                      6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM B).
MEDIINE-97197836; Pubmed-9045686;
Vincenz C., Dixit V.M.;
Fas-associated death domain protein interleukin-lbeta-converting enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICEA_HUMAN STANDARD; PRT; 521 AA.
09281; 08WYQ8; 099845; 09Y2U6; 09Y2U7;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 4)
Apoptotic protease Mch-4) (FAS-associated death domain protein interleukin-la-converting enzyme 2) (FLICE2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains."; Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomaselli K.J.,
        Query Match .16.6%; Score 410; DB 1; Length 479; Best Local Similarity 26.1%; Pred. No. 2.1e-18; Matches 137; Conservative 106; Mismatches 172; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                        -RKRPLLDLHIELNGYMYDWNSRVSAKE--KYYVWLQHTLRKKLI 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| :| || || || || || 434 PRGDDILTILTEVN---YEVSNKDDKKNMGKQMPQPTFTLRKKLV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-T-cell;
MEDLINE-96553838; PubMed-8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J.,
Wang Lilrich F., Fritz L.C., Trapani J.A.,
Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Name=C; Synonyms=10-C;
ISOId=092851-3; Sequence=VSP_000821, VSP_000822;
-1- TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION
IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.
-1- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
THE TWO ACTIVE SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND
TWRR-1 RECEPTORS IN A FADD DEPENDENT WANNER. WAY PARTICIPATE IN
THE GRANZYME B APOPTOTIC PATHWAYS. CLEAVES AND ATIVATES CASPASE-
3, -4, -6, -7, -8, AND -9, HYDROLYZES THE SWALL- MOLECULE
SUBSTRATES, TYR-VAL-ALA-ASP-|-AMC AND ASP-GLU-VAL-ASP-|-AMC.
-!-FUNCTION: ISOPONME C IS PROTEOLYTICALLY INACTIVE.
-!-SUBULT: HETERODIMER OF A 23/17 kDa (P23/17) DEPENDING ON THE
SPLICING EVENTS AND A 12 kDa (P12) SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda J.-E., Hayden M.R.; "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2) cartitical region at chromosome 2q33-q34: candidate genes for ALS2."; Genomics 71:200-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99339325; PubMed-10412980; Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X., Puck J.M., Straus S.E., Lenardo M.J.; Inherited human caspase 10 mutations underlie defective lymphocyte and dendritic cell apoptosis in autoimmune lymphoproliferative syndrome type II.; Cell 98:47-58(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1 protease Moh5 is a CrmA-inhibitable protease that activates multiple Ced 3/ICE-11ke cysteine proteases."; Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
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-!- SIMILARITY: BELONGS TO PEPPIDASE FAMILY C14.
-!- SIMILARITY: Contains 2 death effector (DED) domains.
                                                                                                                                                                 TISSUE-Spleen, and Thymus; MEDLINE-99214592; PubMed-10187817; NG P.W., Porter A.G., Janicke R.U.; "Molecular cloning and characterization of two novel pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
:
                                                                                                                                 (ISOFORMS B AND C), AND VARIANT ILE-410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack
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Name=A; Synonyms=10-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
95- and p55-mediated death signaling.";
Biol. Chem. 272:6578-6583(1997).
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Name=B; Synonyms=10-B;
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MEDLINE-21100893; PubMed-11161814;
                                                                                                                                                                                                                                                                                                                                                 isoforms of caspase-10.";
J. Biol. Chem. 274:10301-10308(1999).
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                                                                                                                        SEQUENCE FROM N.A.
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27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82
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MEDLINE-96325459; Pubmed-8670425;
                                                                                                                                                                                                                                                                                                              442 LHIELNG 448
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BY SIMILARITY.
BY SIMILARITY.
Missing (in isoform B).
/FIId-VSP_000819.
MIKFLEKTMEIRGERKTVWGARQISATSLPTAISAQTPRPP
MRRWSSVS -> HEDILSILTAVNDDVSRRVDKQGTKKQMP
OPAFTLEKKLVFPVPLDALSI (in isoform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG-VSP_000820.
GNRAINGAPSLVSRGMQGASANILNSETSTKRA -> EGSC
VQDESEPQRPLCHCQQPQLYLPEGGTRNP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVGD---LAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.1%; Score 323.5; DB 1; Length 521; Best Local Similarity 26.9%; Pred. No. 5.2e-13; Matches 131; Conservative 77; Mismatches 204; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                            CASPASE-10 SUBUNIT P23/17.
CASPASE-10 SUBUNIT P12.
DED 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> G (IN REF. 2).
->*A (IN REF. 3).
840348AE602B8243 CRC64;
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PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
HYDROSITE; PS50168; DED; 2.
Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat; Alternative splicing; Polymorphism; Disease mutation.
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/FIId-VSP_000822.
L -> F (IN ALPS2).
/FIId-VAR_014071.
V -> I
                                                                                                                                                                                                                   GO; GO:0004199; F:caspase activity; TAS.
GO; GO:0004206; F:caspase-10 activity; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
InterPro; IPR001875; DED.
InterPro; IPR002398; ICE.
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Pfam; PF00656; Peptidase_C14; 1.
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InterPro; IPR001309; ICE_p20.
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SWART; SW00115; CASc; 1.
SWART; SW00031; DED; 2.
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521 AA;
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CONFLICT
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HSSP;
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141 SLPK----TEMTSLSFLAFLEKQGKIDEDNLTCLEDLCKTVVPKLLRNIEKYRREKAIQI 196
                                         119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLE------KCLKNIHRIDLKTKIQ- 169
                                                                                                                                                                                                                                                                                                                   -----KYKQSVQG-----AGTSYRNVLQAAIQKSLKDP----SNNFRLHNGRSKEQRLKE 215
                                                                                                                                                                                                                                                                                                                                                                    197 VTPPVDKEAESYQGEEELVSQIDVKIFLEALPQESWQNKHAGSNGNRATNG-APSLVSRG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 PTSLQD----SIPAEADFLLGLATVPGYVSFRHVEEGSWYIQSLCNHLKKLVPRMLKFLE 478
LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 MOGASANTLNSETSTKRAAV-----YRMNRNHRGLCVIVNNHSFTSLKDRQGTHKDA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 QLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLII------DCIG--NET
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Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
"A random DNA sequencing, computer-based approach for the generation
of a gene map of molluscum contagiosum virus.";
Virus Genes 14:73-80(1997).
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Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
Neipel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M.,
Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.;
"Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159L OR H-H2.2.
Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  098325; 011298;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral
FLICE-inhibitory protein) (v-FLIP).
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MEDLINE-97352177; PubMed-9208457;
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death receptors.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                         (DISC) FORMED BY TWFRSF6, FADD AND CASPASE-8. INTERACTS WITH FADD. SIMILARITY: Contains 2 death effector (DED) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSL-IFL--MKDYMGRG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 KISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGTSYR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 NVLQAAIQKSLKDPSNNFRLHNGRSKEQRL---KEQLGAQQEPVKKSIQESEAFLPQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                poxvirus proteins
                                     Banks
                          MEDLINE-97188440; PubMed-9037025; Bark Bark Armstrong R.C., Ottilie S., Martin D.A., Wang Y., Bank Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J., Tomaselli K.J., Cohen J.I.; Alnemri E.S., Moss B., Lenardo M.J., Tomaselli K.J., Cohen J.I.; Death effector domain-containing herpesvirus and poxvirus protei inhabit both Fas- and THRR-induced apoptosis."; Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
                                                                                                                                                                                                                  SUBUNIT: ASSOCIATES WITH THE DEATH-INDUCING SIGNALING COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 231.5; DB 1; Length 241; 30.4%; Pred. No. 9.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA; 26939 MW; 155C9FB0B969E216 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Mismatches
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                                                                                                             MEDLINE-99457304; PubMed-10526240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICE6_HUMAN STANDARD;
P55212; Q9BQE7;
01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                 EMBL; U60315; AAC55287.1; -. EMBL; U86888; AAB57923.1; -.
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO1875; DED. Pfam; PF01315; DED; 2. SMART; SM0031; DED; 2. PROSITE; PS50168; DED; 2. Apoptosis; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Conservative
Nature 386:517-521(1997)
                                                                                                                                                                                                                                                                                                                                            EMBL; U86888; AAB57
PIR; T30761; T30761
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                    CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L., Feinglüßer. S., Wagner L., Shemmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A. Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Haieh F., Stateleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Josens M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Brownstein M.J., Usdin T.B., Tooshiyuti S., Carninci P., Prange C., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Mortigle Y.S.N., Krayminski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial malysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT-
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId-P5512-2; Sequence-VSP_000805;
-1- PIM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fernandes-Alnemri T., Litwack G., Alnemri E.S.; Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alnemri \bar{E}.S.; "The Ced-3/interleukin lbeta converting enzyme-like homolog Mch6 and the Lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mediator CPP32.";
J. Biol. Chem. 271:27099-27106(1996).
J. Biol. Chem. 271:27099-27106(1996).
I. FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
PROGRAMMED CELL DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lymphocytes;
MEDLINE-97059171; PubMed-8900201;
Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
                                                                                                                                                                                                                          Euteleostom1;
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEB-2003 (Rel. 42, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
CASP6 OR MCH2.
                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-P55212-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-T-cell;
MEDLINE-95316841; PubMed-7796396;
Fernandes-Alnemri T., Litwack G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Res. 55:2737-2742(1995).
                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Alpha;
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 29.4 67; Conservative
            Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                   P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                            MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339
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                                         SEQUENCE
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SEQUENCE
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EENWIETDAFYKREMFDPAEKYKMDHRRGIALIFNHERFFWHLTLPERRGTCADRDN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRDTFTSLGYEVQKF-----LHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 HIYAYDAKIELQTLTGL-----FKGDKCHSLVGKPKIFILQACRGNQHDVPVIPLDV
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3) (CASP-3) (ACPP32).
                                                                                                                                                                                                                                                                                                                                                                                                  74; Gaps
                                                                                                                                                                 Pfam; PF00655; ICE_pl0; 1.
Pfam; PF00655; ICE_pl0; 1.
PRINTS; PR00376; ILLBCENZYME.
SWART; SM00115; CASFASE_CYS; 1.
PROSITE; PS01122; CASFASE_HIS; 1.
PROSITE; PS01020; CASFASE_Pl0; 1.
PROSITE; PS50207 CASFASE_Pl0; 1.
Hydrolase; Thiol procease; Apoptosis; Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVYGVD-----QTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ------
                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 192; DB 1; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                  74; Indels
                                                                                                                                                                                                                                                                                           CASPASE-6 SUBUNIT P11.
BY SIMILARITY.
BY SIMILARITY.
MISSING (In 1soform Beta).
//TIG-VSD.000805.
G - R (IN REF. 1).
W; 0738AE4F9791EBD7 CRC64;
                                                                                              MIM; 601532; -. 605.008234; F:cysteine-type peptidase activity; TAS. 60; 60:0008234; P:protection of apoptosis; TAS. 60; 60:0006508; P:proteclysis and peptidolysis; TAS. InterPro; IPR002398; ICE_p10. InterPro; IPR00138; ICE_p10. InterPro; IPR001389; ICE_p10.
                                                                                                                                                                                                                                                                          CASPASE-6 SUBUNIT P18
                                                                                                                                                                                                                                                                                                                                                                                      25.9%; Pred. No. 3.5e-05; ive 38; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 AA
 email to license@isb-sib.ch).
                              U20537; AAC50169.1; -. BC000305; AAH00305.1; -. BC004460; AAH04460.1; -.
                                                                                                                                                                                                                                                                                                                                                           33310 MW;
                     EMBL; U20536; AAC50168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Similarity 25.99 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLYLOCLSOKL 431
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                                                                                   HGNC:1507; CASP6.
                                                            HSSP; P42574; 1PAU.
MEROPS; C14.005; -.
Genew; HGNC:1507; CA.
                                                                                                                                                                                                                                                                                                                                                           293 AA;
                                                                                             601532;
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P55866;
  or send an
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ACT_SITE
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 LSMHGISQILGQFACMPE--HRDYDSFVCVLVSRGGSQ-SVYGVDQTHSGLPLH--HIRR 338
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                                                                                           Yaoita Y., Nakajima K.;

Yaoita Y., Nakajima K.;

"Induction of apoptosis and CPP32 expression by thyroid hormone in a myoblastic cell line derived from tadpole tail.";

"Induction of apoptosis and CPP32 expression by thyroid hormone in a myoblastic cell line derived from tadpole tail.";

"Induction of apoptosis and CPP3."

"Induction of apoptosis and CPP3."

"Induction in All ST 12.51.27-51.27 1907.

"Induction in All ST 12.51.27 1807.

"Induction in All ST 15.51.27 1807.

"Induction in All ST 15.51.27 1807.

"Induction in All ST 15.51.27 1807.

"Induction in All ST 21.51.27 1807.

"Induction in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDLHIEL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 ADFLYAYSTVPGYCSWRDKMDGSWFIQSLCKMIK-----LYGSHLEL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 191.5; DB 1; Length; 29.4%; Pred. No. 3.6e-05; ve 34; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

BY SIMILARITY.

CB390E6980CAB77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0021399; ICE.
InterPro; IPR0021399; ICE.
InterPro; IPR0021399; ICE.P10.
InterPro; IPR001309; ICE.P20.
PRINTS; PR00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBCENZYME.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HS; 1.
PROSITE; PS01020; CASPASE_HS; 1.
PROSITE; PS020070; CASPASE_P10; 1.
PROSITE; PS020070; CASPASE_P10; 1.
PROGIE; PS020070; CASPASE_P10; 1.
PROGIES; PS020070; CASPASE_P10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APOPAIN P17 SUBUNIT APOPAIN P12 SUBUNIT
SEQUENCE FROM N.A.
MEDLINE-97184166; PubMed-9030578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 AA; 32124 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D89784; BAA14018.1; -.
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448 GYMYD------WNSRVSAKEKYYVW 466
                                                                                                                                                                                                                    | : :|:|::
SLFKDKCPNSRSQMPTQERCTLTKKFYLF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=098943-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note-Only form found in the ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U64963; AAC29881.1; ALT_INIT.
HSSP; P42574; ICP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IIIBCENZYME.
SMART; SM00114; CARD; 1.
SNART; SM00115; CARD; 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001315; CARD.
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C14.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ICH-1S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASP2 OR ICH1.
                                                                                                                                                                                                                                                                                                                                           CHICK
                                                                                                                                                296
                                                                                                                                                                                                                                    355
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                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 DLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGTSYRNVLQAAIQK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DKIYDVRKREGRKGLALII-CNEKFENLNERHGAKVDLDGMTKLLNE----LGYQVHPH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 LHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVD-------QTHSG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 SLKDPSNNFRLHN------GRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IGNETELLRDIFISLGYEVORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 NHKTLAKSLGLHEPPMAPVPIQEHNADTIKNKDIKGVIPCSAEEFKK-IQDTQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mphlibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-1 beta convertase homolog A precursor (EC 3.4.22.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.7%; Score 190.5; DB 1; Length 386; 21.9%; Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                 Yaoita Y., Nakajima K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
--- SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y SIMILARITY.
Y SIMILARITY.
927C71FC9FED79E6 CRC64;
386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 PEERYKMKSKP--LGICLIIDC------
                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0376; ILIBEENZYME.
SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_INS; 1.
PROSITE; PS01121; CASPASE_INS; 1.
PROSITE; PS01012; CASPASE_INS; 1.
PROSITE; PS50209; CASPASE_P10; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001315; CARD.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PP00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
                                                                                                                      (XICE-A) (Caspase-1A) (CASP-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA; 43663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D89783; BAA14017.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; C14.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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Matches
HID DESTRUCTION OF THE PRINCE 
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LPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQLENSSLL--EVDGPAMKNVEFKAQ 388
                                                                                                                                                                                   447
                                                                                                                                                                                                                                        - DGLHFVQREADFICECSSTPDIVSWRDPTKGSVFITHLIEKMNEYAHCQPLGDIFLEVQ 354
                                                                                                                                                                         389 KRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ-ERKRPLLDLHIELN
                                                                             245 LEIDEIFSTFNNVNCSKLRNKPKVIIIQ----ACRGENKGGLLVRDDVASPPLED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA in the hen ovary.";
Gene 192:227-233(1997).
-I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION, MIGHT FUNCTION BY EITHER
ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=088943-2; Sequence=VSP_000803, VSP_000804;
-1- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-White leghorn; TISSUE-Ovarian granulosa;
BEDLINE-2758127; PubMed-9224884;
Johnson A.L., Bridgham J.T., Bergeron L., Yuan J.;
"Characterization of the avian Ich-1 cDNA and expression of Ich-1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA.
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147
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                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                             72
                                                                                                                          /FTId=VSP_000803
DEPDRGVDQROKERESDSPCGEESDANKEBNLKLRLPTRSD
MICGYGLIKGTAARRHTRGSWYIBALTTYVBAEDSRDTHVA
DMLVKVNRQIKQREGYAPGTEFHRCKEMSBYCSTLCRDLYL
                                                                                                                                                               FPGYVPGK -> GVSGIHIHLPLPCCCHCICCSMRQTGEWI
REMAKNGQIPQAVRRVMQTRKKISSCVCLHAPI (in
                                                                                                                                                                                                                                                                     94 RVLMA-----EIGEDLDKSDVSSLIFILMKDYMGRGKISKEKSFLDLVVELEKLNLVAPD
                                                                                                                                                                                                                                                                                                                                                                          ----IDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEH
                                                                                                                                                                                                                                                                                                                                                                                          181 FSSEKDLEYRSGGDVDCA--SLELL---FKHLGYQVTVFHDQSAEEMESALERFSKLPDH
                                                                                                                                                                                                                                                                                              148 QLDLLEKCLKNIHRIDLKTKIQKYKQSVQ-GAGT---SYRNVLQAAIQKSLKDPSNNFRL
                                                                                                                                                                                                                                                                                                                 73 AFSAFCEALQETKQQHLAEMILKTESSLRHGIATLEQRYGSNLPLPLSESC-----
                                                                                                                                                                                                                                                                                                                                    204 HNGRSKEQRL--KEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLI----
                                                                                                                                                                                                                                                                                                                                                                                                              RDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                        SIMILARITY).
SIMILARITY).
SIMILARITY).
                                      protease; Apoptosis; Zymogen; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICE3_HUMAN STANDARD; PRT; 277 AA.
P42574; Q96AN1; Q96KP2;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
"CPB32, a novel human apoptoric protein with homology to Caenorhabditis elegans cell death protein Ced-3 and mammalian Interleukin-1 beta-converting enzyme.";
J. Biol. Chem. 269:30761-30764(1994).
                                                                                                                                                                                                                      Length 424;
                                                                                                                                                                                                                                Pred. No. 8.5e-05;
43; Mismatches 121; Indels
                                                                                                                (in isoform ICH-1S). P_000803.
                                                         (BY
(BY
(BY
                                                                                                                                                                                                 792810508BBBZF60 CRC64;
                                                        CASPASE-2 SUBUNIT P18
CASPASE-2 SUBUNIT P13
CASPASE-2 SUBUNIT P12
                                                                                                                                                                                                                      Score 189; DB 1;
Pred. No. 8.5e-05;
                                                                                                                                                                                          000804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                  isoform ICH-1S
                                                                                               SIMILARITY
                                                BY SIMILARITY
                                                                                                         SIMILARITY
                                                                                                                                                                                           /FTId~VSP.
                                                                                              BY SIMILA
BY SIMILA
Missing (
CASPASE_CYS; 1.
CASPASE_HIS; 1.
CASPASE_P10; 1.
CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95074098; PubMed-7983002;
                                                                                                                                                                                                   47959 MW;
                                                                                                                                                                                                                              Best Local Similarity 25.79
Matches 76; Conservative
                                                                           424
96
                                                                                              248
291
                                                                 424
                                                                                                                                   424
                                                                                                                                                                                                   424 AA;
                  PROSITE; PS50207;
PROSITE; PS50208;
                                      Thiol
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CASP3 OR CPP32.
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                                     Hydrolase;
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ACT_SITE
ACT_SITE
VARSPLIC
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SEQUENCE FROM N.A.
MEDLINE-95292347; PubMed=7774019;
Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
"Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease that cleaves the death substrate poly(ADP-ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.K.
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MEDLINE=20283632; PubMed=10821855;
Libe D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
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Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
                                                                                                                                                                                                                                                                                                            Vallette F.M., Oliver L.J.;
"Control of the activation of the procaspase-3 by a sequence located at the N-terminus of the p17 subunit."; at the N-terminus of the p17 subunit."; bbmt(SEP-2001) to the EMBL/GenBank/DDBJ databases..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller D.K.;
Identification and inhibition of the ICE/CED-3 protease necessary
for mammalian apoptosis.";
Nature 376:37-43(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding
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Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97197830; Pubmed-9045680;
Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S. Priestle J.P., Tomaselli K.J., Grutter M.G.;
"Structure of recombinant human CPP32 in complex with the tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
J. Biol. Chem. 272:6539-6547(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=96266352; PubMed=867360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM BETA)
                                                                                                                                                                                           polymerase.";
Cell 81:801-809(1995).
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; GO:0004208; F:caspase-3 activity; TAS.
GO:0008624; P:induction of apoptosis by extracellular sig. . .; TAS.
GO:0008629; P:induction of apoptosis by intracellular sig. . .; TAS.
GO: GO:0009405; P:pathogenesis; TAS.
                                                  MEDLINE=96553838; PubMed=8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.; and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains."; Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
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                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002398; ICE.
InterPro; IPR0012138; ICE_D10.
InterPro; IPR001309; ICE_D20.
Pfam; PF00656; Peptidase_L14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U13737; AAA65015.1; -.
EMBL; U13738; AAB60355.1; -.
EMBL; U26943; AAA74929.1; -.
EMBL; AA413269; CAC88866.1; -.
EMBL; EMBL; AA416926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:1504; CASP3.
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PDB; 1PAU; 07-JUL-97.
PDB; 1CP3; 24-DEC-97.
PDB; 1GFW; 23-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; C14.003; -. Genew; HGNC:1504; C7 MIM; 600636; -.
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328 HSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQ--LENSSLLEVDGPAMKNVEF 385
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P70677; 008668; 090M14;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
CASP3 OR CPP32.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
SMART; SM00115; CASC: 1.

PROSITE; PS01122; CASCASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; 1.

PROSITE; PS50207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

HydroLase; Thiol protease; Zymogen; Apoptosis; Polymorphism; 3D-structure.
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D -> E (IN ISOPORM BETA).

/FIId-VAR 001401.

ISLDNS -> MSWDTG (IN REF. 3).
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26.8%; Pred. No. 0.00016;
tive 40; Mismatches 102;
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APOPAIN P12 SUBUNIT.
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Best Local Similarity 26.8%
Matches 69; Conservative
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modified and this statement is not removed. Usage by and for commercial
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Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,

R Fortin J.-P., Sekaly R.-P.;

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Multiple pathways of apoptosis converging on the CPP32 protease.";

"Lisubmitted (JUL-1996) to the EMBL/GenBank/DDBJ databases

"In FREPORSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF RAPOPTOSIS IT PROTEOLYTICALLY CLEAVES AND ACTIVATES AND ACTIVATES STEROL REGULATORY

CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

CLEAVES IL-1 BETA BETWEEN AND AN ALA, RELEASING THE MATURE CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.

C -1- SUBUNIT: HETERODIMES OF A 17 KDB (P17) AND A 12 KDB (P12) SUBUNIT CHOCKETHY AND ALCHARACTORY PROCESSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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SEQUENCE FROM N.A.
MEDLINE-96358624; PubMed-8761296;
Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE-9724429; bubmed-9070890;
MEDILINE-9724429; bubmed-mori M.Y., Kimura I., Momol T.;
Mikasa T., Urase K., Momol M.Y., Kimura I., Momol T.;
Mikasa T., Crase K., Momol M.Y., Kimura I., Momol T.;
Mikasa T., Urase R., Momol M.Y., Kimura I., Momol T.;
Mikasa T., Momol M.Y., Kimura I., Momol T.;
Mikasa T., Momol M.Y., Kimura I., Momol T., Momol M., Momol M., Mikasa I., Momol M., Momol
                                                                                                                                        "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCARALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C3H/An;
MEDLINE-97190206; PubMed-9038361;
Wan de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seven murine caspase family members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of seven r
FEBS Lett. 403:61-69(1997).
                                                                                                                                                                                                                                                  Oncogene 13:749-755(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U49929; AAC52764.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC53196.1;
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                                                                                                          Fletcher F.A.;
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271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 MGLKYQVRNKNDLTREDILELMDSVS-KEDHSKRSSFVCVILSHGDEGVIYG---INGPV
                                                                                                                                                                                                                                                                                                                                                                                                                            226 KSIQESEAFLPQSIPEERYKWKSKPLGICLIID------CIGNETEL--LRDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
Apopain precursor (C. 3. 4.22. -) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                              CE91598F74826605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 LCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 432
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REF. 2).
                                                                                                                                                                                                 APOPAIN P12 SUBUNIT.
APOPAIN P12 SUBUNIT.
BY SIMILARITY.
E -> G (IN REF. 2).
N -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                        88;
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29.0%; Pred. No. 0.00017;
ive 34; Mismatches 88
                                                                                                                                                                                                                                                                                                                                       (IN REF. 5)
                                                                                                                                                                  Thiol protease; Zymogen; Apoptosis.

1 9 BY SIMILARITY.

10 28 BY SIMILARITY.
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Q -> E
D -> E
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                               MEROPS; C14.003; MEROPS; MGD; MGD; MGID; MGII,07739; Casp3.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_D10.
InterPro; IPR001309; ICE_D20.
Pfam; PP00656; Peptidase_C14; I.
PRINTS; PR00376; ILIBGENZYME.
                                                                                                                     PROSITE; PS01122; CASPASE_CYS; 1. PROSITE; PS01121; CASPASE_HIS; 1. PROSITE; PS50207; CASPASE_P10; 1. PROSITE; PS50208; CASPASE_P20; 1. Hydrolase; Thiol protease; Zymoge
                                                                                                                                                                                                                                                                                                                                                              31474 MW;
EMBL; U63720; AAD09504.1;
PIR; JC5410; JC5410.
HSSP; P42574; 1PAU.
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                                                                                                             SMART; SM00115; CASC; 1
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175
121
163
17
163
17
163
95
84
95
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277 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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CASP3 OR CPP32.
                                                                                                                                                                                                                                                                                                                                                                                     Local 5...
64;
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Q60431;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 PLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQ--LENSSLLEVDGPAMKNVEFKAQK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 TSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                             Goldstein J.L.;

"Cleavage of sterol regulatory element binding proteins (SREBPS) by
"Cleavage of sterol regulatory element binding proteins (SREBPS) by
EMBO J. 15:1012-1020(1996).

-I FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE OWNET OF APOPTOSIS IT
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-I-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES AND ACTIVATES CASPASE 6, -7 AND -9 (BY SIMILARITY).

-1- SUBUNIT: HETERODIMBER OF A 17 KDB (P17) AND A 12 KDB (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSIQESEAFLPQSIPEERYKMKSKPLGICLIID------CIGNETEL--LRDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYtoplasmic.
PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
PROPEASE. ACTIVE HETENDIMENS BETWEEN THE SMALL SUBUNIT OF
CASPASE-7 PROFEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 RGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 432
                                 ., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBF3A4590A2828A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOPAIN P17 SUBUNIT. APOPAIN P12 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00022;
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1 9 BY SIMILARITY.

10 28 BY SIMILARITY.
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Mismatches
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                 PubMed=8605870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002399; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBCENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO1122; CASPASE_CYS; 1. PROSITE; PSO1121; CASPASE_HIS; 1. PROSITE; PS50207; CASPASE_P10; 1. PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31612 MW;
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Conservative
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176
121
163
277 AA;
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ACT_SITE
SEQUENCE
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                                 Wang X
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MEDLINE-96358624; PubMed-8761296;
Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle.";
Endocrinology 136:5042-5053(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBDITICE (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-- PUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION: AT THE ONSET OF APOPTOSIS IT
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-|-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELLY-LCOPP-
HELLY LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

-- SIBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWO ACTIVE SUBURITS. ADDITIONAL PROCESSING OF THE PROPERTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBURIT OF CASPASE-7 PROTEASE AND THE LARGE SUBURIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE BUT NOT IN KIDNEY OR TESTIS.

-1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED RECIONS OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
Rosteck P. Jr., Poirler G.G., Paul S.M.;
"Cloning and expression of a rat brain interleukin-lbeta-converting
enzyme (ICE)-related protease (IRP) and its possible role in
apoptosis of cultured cerebellar granule neurons.";
J. Neurosci. 17:1561-1569(1997).
                                                                                                                  P55213, P70543; P70543; P70593; O1-0CT-1996 (Rel. 34, Created)
O1-0CT-1996 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama Protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
CASP3 OR CPP32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;
  ----IPVEADFLYAYSTAPGYYSWRNPKDGSWFIQSLCSMLK 224
                                                                                                       277
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Ovary;
MEDLINE-96042508; PubMed-7588240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 30-241 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 13:749-755(1996).
                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADULT BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yakovlev A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fletcher F.A.
187
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                              RESULT 14
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BY SIMILARITY.
APOPAIN P17 SUBUNIT.
APOPAIN P12 SUBUNIT.
       SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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25.7%; Pred. No. 0.00
tive 38; Mismatches
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BY SIMILARITY
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InterPro; IPR002398; ICE_pl0.
InterPro; IPR001318; ICE_pl0.
InterPro; IPR001309; ICE_pl0.
InterPro; IPR001309; ICE_pl0.
InterPro; IPR001309; ICE_pl0.
INTERPROSTOR; ILIBERNZYME.
SMART; SM00115; CASC; 1.
IPROSTOR; PS01122; CASPASE_HIS; 1.
PROSTOR; PS50207; CASPASE_HIS; 1.
INTERPROSTOR; INTERPROSTOR INTERP
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212 GSWFIQSLCAMLK 224
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277 AA;
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wes 65; Conserv
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RESULT 15 ICE2_MOUSE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).

TISSUE SPECIFICITY: HIGH LEVEL EXPRESSION SEEN IN THE EMBRYONIC CNS, LIVER, LUNG, KIDNEY, SMALL INTESTINE, AND HARR FOLLICLES OF VIBRISSAE. MODERATE EXPRESSION SEEN IN THE SKIN, ORAL MUCCSA, SKELETAL MUSCLE, SUBMANDIBULAR GLAND AND THYMGS. IN THE ADULT, IT IS HIGHLY EXPRESSED IN SPLEEN, LOW LEVELS IN THE THYMGS. IN THE ABOULT, LONG AND KIDNEY. MODERATELY IN THE MUSCLE, OVARY AND GUT.

DEVELOPMENTAL STAGE: DURING EMBRYONIC DEVELOPMENT IS HIGHLY EXPRESSED IN SEVERAL TYPES OF MOUSE TISSUE UNDERGOING HIGH RATES OF PROGRAMMED CELL DEATH SUCH AS CENTRAL NERVOUS SYSTEM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPERTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: Contains I CARD domain.
             P29594; 008737;
01.APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C3H/An;
MEDLINE=97190206; PubMed=9038361;
Van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
Van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                 STRAIN-BALB/C;
MEDLINE-95647319; PubMed=7958843;
Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
Kumar S., Kinoshita M., Noda M., Copeland S.G., Jenkins N.A.;
Induction of apoptosis by the mouse Nedd2 gene, which encodes a protein similar to the product of the Caenorhabditis elegans cell death gene ced-3 and the mammallan IL-1 beta-converting enzyme.";
Genes Dev. 8:1613-1626(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of seven murine caspase family members."; FEBS Lett. 403:61-69(1997).
435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D28492; BAA25876.1; ALT_INIT.
EMBL; Y13085; CAA73527.1; ALT_INIT.
HSSP; P42574.1 CP3.
MEROPS; C14.006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92328780; PubMed-1378265;
                                                                                                        protein). CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
 STANDARD;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=10090;
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84 LRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNL 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 PSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLI 256
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22.6%; Pred. No. 0.00052;
tive 63; Mismatches 167; Indels 105; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASPASE-2 SUBUNIT P18 (BY SIMILARITY)
CASPASE-2 SUBUNIT P13 (BY SIMILARITY)
CASPASE-2 SUBUNIT P12 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SINILARITY.

C->G: LOSS OF FUNCTION.

MISSING (IN REF. 1).

W; 8984E6AA76E7A676 CRC64;
               InterPro; IPR00115; CARD.
InterPro; IPR0012199; ICE.
InterPro; IPR0012199; ICE.
InterPro; IPR0012199; ICE.
InterPro; IPR0012199; ICE.
InterPro; IPR001309; ICE.
INTER; IPR00114; CARD; I.
INTER; IPR00115; CASC; I.
IPR0SITE; PS01121; CASPASE_HIS; I.
IPR0SITE; PS01201; CASPASE_P20; I.
IPR0SITE; PS012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 13, 2003, 16:40:19 Job time : 21.5421 secs
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391 VKVNALIKEREGY 403
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Matches 98; Conserv
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ACT_SITE
ACT_SITE
MUTAGEN
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· Mon Aug 25 09:11:04 2003

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 13, 2003, 16:40:24; Search time 28.7589 Seconds (without alignments) 706.188 Million cell updates/sec Run on:

US-09-380-546A-2 2473 1 MSAEVIHQVEEALDTDEKEM.......EKYYVWLQHTLRKKLILSYT 480 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*
 // Cgn2_6/ptodata/1/laa/5A_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/5B_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/6A_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/BaCB_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
 // Cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	-795-088A-2 Sequence 2, Appli	4 Seguence 34.	Sequence 2.		7	Sequence	7 Sequence 17,	7 Sequence 17,	'n	Sequence 7,	7 Sequence 7,	7 Sequence 7,	7	-12 Sequence 12,	Sequence 3,	Sequence 1	8 Sequence 18,	18 Sequence 18,	Sequence 2, A	Sequence 28,	Sequence 27,	Sequence 28,	Seguence 26,	7 Sequence 27,	6 Sequence 26,		374-044A-1 Sequence 1.
SUM	ID	-80-SD	-60-sn	-80-SD	-60-SD	-60-Sn	-60-sn	-60-sn	-60-Sn	-60-Sn	-80-SD	-60-sn	PCT-US	ns-08-	-60-SN	ns-08-	-80-sn	-60-Sn	PCT-US	-60-Sn	-60-sn	-60-sn	-60-SD		9	-09	-08	ns-09-(
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ď	Query Match	99.8	97.5	91.6	91.6	91.6	91.6	40.7	40.7		16.6	16.6	16.6	16.5	16.5	16.4	16.4	16.4	16.4	16.3	16.3	16.3	16.3	16.2	16.1	•	15.5	15.5
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Gaps ö

Length 480; Indels

Query Match
99.8%; Score 2468; DB 3;
Best Local Similarity 99.8%; Pred. No. 1.2e-230;
Matches 479; Conservative 1; Mismatches 0;

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1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 

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61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Sequence 4, Appli Sequence 2, Appli Sequence 27, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 2, Appli		
28 381.5 15.4 496 1 US-08-665-220-4 29 381.5 15.4 496 3 US-09-291-622-4 30 370.5 15.0 476 4 US-09-561-756-27 31 370.5 15.0 476 4 US-09-551-756-27 32 323.5 13.1 521 4 US-09-665-220-2 34 318.5 12.9 479 1 US-08-665-220-2 35 318.5 12.9 479 1 US-08-665-220-2 36 318.5 12.9 479 4 US-09-291-622-2 37 318.5 12.9 479 4 US-09-561-756-33 38 274 11.1 335 4 US-09-561-76-16 40 246 9.9 389 4 US-09-510-77-16 41 246.5 10.0 286 4 US-09-360-107-1 42 231.5 9.4 241 3 US-09-382-155-21 44 231.5 9.4 241 3 US-09-074-044A-21	ALIGNMENTS	RESULT 1 US-08-795-088A-2 Sequence 2, Application US/0879508BA Fatent No. 624256 GENEMAL INCRMATION: APPLICANT: Sul, Hong-Bing APPLICANT: Sul, Hong-Bing APPLICANT: Gooddel, David V. TILLE OF INVENTION: Regulators of Apoptosis NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: Science & Technology Law Group STREET: 75 Denise Drive CITY: Hillsborough STRATE: California COUNTRY: USA ZIP: 94010 COMPUTER: IBM PC compatible COUNTRY: USA ZIP: 94010 COMPUTER: Plan PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,088A FILING DATE: CLASSIFICATION: 435 ATCRNEY/AGENT INFORMATION: NAME: OSMAN, Richard A RECISTRATION NUMBER: 36,627 ATCRNEY/AGENT INFORMATION: TELEPOMMUTCATION INFORMATION: TELEPOMMUTCATION INFORMATION: TELEPOMMUTCATION NUMBER: 197-001 TELEPAX: (650) 343-4341 TELEFAX: (650) 343-4341

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ZIP: 1913
ZIP: 1913
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WOATDEATECT
CURRENT APPLICATION NUMBER: US/08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNDRER: 33,229
REFERENCE/DOCKET UNDRER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.6%;
92.5%;
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Best Local Similarity 92.5
Matches 444; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-859-167-2
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Batent No. 6348573

GENERAL INFORMATION

APPLICANT: Nunez, Gabriel

APPLICANT: Roseki, Takeyoshi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILLE REFERENCE: UM-03333

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PATENTING VET. 2.0

SEQ ID NO 344
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Pred. No. 3.3e-225;
3; Mismatches 8; Indels
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Matches 469; Conservative
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US-09-069-023-34
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                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08859167
Patent No. 6037461
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Farnandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: Of MAKING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: ADDRESSES:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                  VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
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Pred. No. 4.6e-211;
1; Mismatches 0;
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Page

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265 360 325

205

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181 SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: Whiladelphia
STREET: Philadelphia
STATE: PA
                                                                                                                                           SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09276993 Patent No. 6207801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 1JU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alnemri, Emad S. APPLICANT: Fernandez-Alnemri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-276-993-2
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                      61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                      TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris STREET: One Liberty Place, 46th floor
                                                                                                    EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY
                                                                                                                                                                      VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP
                                 EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP
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Pred. No. 4.6e-211;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
SYRNVLQAAIQKSLKDPSNNFR-
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alnemri, Emad S. APPLICANT: Fernandez-Alnemri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBL OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.6%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
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APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILLE REPERBENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT APPLICATION NUMBER: 09/074,044
EARLIER PLING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 40
                             EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360
    61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
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                                                                                                                                            EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP
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Pred. No. 1.5e-89;
1; Mismatches 0;
                                                                                                      SYRNVLQAAIQKSLKDPSNNFRL 203
                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 17, Application US/09382155B; Patent No. 6160095; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09074044A
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SEQ ID NO 17
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US-09-382-155-17
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                                                        1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
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Factor No. 6576751

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: Radd-Like Anti-Apoptotic Molecules, Methods Of U TITLE OF INVENTION: Compositions For And Methods Of Making The Same; FILE REFERENCE: TUJ2445

CURRENT APPLICATION NUMBER: US/09/723,450

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR APPLICATION NUMBER: 08/859,167

PRIOR FILING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Version 3.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
Score 2265.5; DB 3; Length 445; Pred. No. 4.6e-211; Mismatches 0; Indels 35;
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Pred. No. 4.6e-211;
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NAME/KEY: misc_feature
OTHER INFORMATION: No. 6576751el Sequence
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 91.6%;
llarity 92.5%;
Conservative
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Best Local Similarity
                Similarity
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    Query Match
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                 Best Local
Matches 44
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26580
TELECOMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE GHARACTERISTICS:
                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOFCLOST:
MOLECULE TYPE: protein
FPAGMENT TYPE: internal
                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                     64108
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ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-074-044A-2
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                                                                       TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
COUNTRY: USA
ZIP: MISSOURI
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
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Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-kB, JNK AND
TITLE OF INVENTION: APPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
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Pred. No. 1.5e-89;
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40.7%; Score 1007; I
Best Local Similarity 99.5%; Pred. No. 1.5e
Matches 202; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
""" FPHONE: 816/474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SYRNVLQAAIQKSLKDPSNNFRL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SYRNVLQAAIQKSLKDPSNNFRM 203
                                    APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not relevant

MILECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
US-09-074-044A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                   GENERAL INFORMATION:
6207458
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US-09-074-044A-2
  Patent No.
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90 VSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQL 149
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Patent No. 6399327
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Tanya M. GONCHAROV
TITLE OF INVENTION: MODILATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
STREET: 2405 GRAND BLVD., SUITE 400
CITYET: ALOS GRAND BLVD., SUITE 400
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%; Score 417; DB 3; 1
100.0%; Pred. No. 5.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Pred. No. 5.3e-
Matches 84; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 DLLEKCLKNIHRIDLKTKIQKYKQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DLLEKCLKNIHRIDLKTKIOKYKO 84
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57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISEEVSRSELRSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI----LRERGKLSVGDLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS AND OTHER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 16.6%; Score 410; DB 4; Length 479; Best Local Similarity 26.1%; Pred. No. 3.9e-31; Matches 137; Conservative 106; Mismatches 172; Indels 110;
434 PRGDDILTILTEVN---YEVSNKDDKKNMGKQMPQPTFTLRKKLV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: ILEM PC COMPATIBLE
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: WALLACH-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DUMBER: 08/983,502
FILING DATE: <UNKNOWN-
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APK-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-516-747-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                           Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-Mar-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                              Sequence 7, Application US/09516747
Patent No. 6586571
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 479 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        APPLICANT: David WALLACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                                                             US-09-516-747-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ-----NY----VVSEGQLENSSLLEVD- 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLQEEISKCKLDDDMNLLDIFIEMEKRVILGEGKLDILKRVCAQINKSLLKI-INDYEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NETEL--- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTTTFEELHFEIKPHDDCTVEQIYEILKIYQLM-DHSNMDCFICCILSHGDKGIIYGTD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPQTRYIP------DEADFILGMATVNNCVSYRNPAEGTWYIOSLCQSLRERC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GPAMKNVEFKAOKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE- 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIGEQLOSEDLASLKFL---SLDYIPQRKQEPIKDALMLEQRKQEKRLGEKNLSFL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI----LRERGKLSVGDLA-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOEA--PIYELTSOFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.9e-31; ; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE,FOCKET NUMBER: WALLACH=19
TELECOMUNICATION INFORMATION:
TELEFAN: (202) 628-5197
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.6%; Score 410; 26.1%; Pred. No. 3
                                            UMBER: PCT/US96/10521
14-JUN-1996
                                                                                                                                                                                                                                                     APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION NUMBER: IL 117,932
APPLICATION NUMBER: IL 117,932
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
                                                                                                                     IL 114,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.6%; Sc
Best Local Similarity 26.1%; Pr
Matches 137; Conservative 106;
                                                                                                                                         FILING DATE: 16-JUL-1995 PRIOR APPLICATION DATA:
DATE: 16-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 479 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-983-502-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOEA--PIYELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 SSPQTRYIP------DEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERC 433
                                                                                                                                                                                                                                                            FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQ 173
                                                                                                                                                                                                                                                                                                                                                                                     -----SVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 -LRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
                                                                                                                                                                 377 -GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE- 434
   6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 56
                                                            7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 SIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIG-------NETEL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08807200
Patent No. 5837837
GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shigjan, Andrew W.
TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELLING ILER.

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FSSISESO, for Windows Version 2.0
CURTERNY APPLICATION DATA:
APPLICATION NUMBER: US/08/807,200
FILING DATE: 27-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/021001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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SIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIG-------NETEL--- 266
                                                                                                                                                                                                                                                        269 ALTITFEELHFEIRPHDDCTVEQIYEILKIYQLM-DHSNWDCFICCILSHGDKGIIYGTD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 QTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ----NY---VVSEGQLENSSLLEVD- 376
                                                                                          ----SVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 -GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE- 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSPQTRYIP------DEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERC 433
                                                                                                                                                                                                                                                                                                                                                   -LRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
16.6%; Score 410; DB 5; Length 479;
Best Local Similarity 26.1%; Pred. No. 3.9e-31;
Matches 137; Conservative 106; Mismatches 172; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 -RKRPLLBLHIELNGYMYDWNSRVSAKE--KYYVWLQHTLRKKLI 476
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NUMBER OF SEQUENCES: 34
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
                                                                                                                                                          181 FSKERSSSLEGSPDEFSNGEELCGVMTISDSPRE-----
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application PC/TUS9610521 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
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FILING DATE: 14-SEP-1995
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FILING DATE: 16-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ----NY---VVSEGQLENSSLLEVD- 376
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                                                                                                                                                                                                                                                                                                                                                                                                                      ----SVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE- 434
                                                                                                                                                                                                                            6 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI----LRERGKLSVGDLA-- 56
                                                                                                                                                                                                                                                  FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQ
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                                                                                                                                                                                               Gaps
                                                                                                                                                                                            Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Carace H.W.
TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND USES THEREOF NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
                                                                                                                                                               Length 479;
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                                                                                                                                                            Query Match 16.5%; Score 408; DB 2; L
Best Local Similarity 26.1%; Pred. No. 6.1e-31;
Matches 137; Conservative 105; Mismatches 173;
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             TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
617-542-8906
                                                                                            TOPOLOGY: 11near

MOLECULE TYPE: protein

US-08-807-200-12
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COUNTRY:
 TELEFAX:
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APPLICANT: Vishva Dixit, Kristine Kikly, Jian Ni, Craig Rosen and APPLICANT: Steven Ruben
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOTIC PR
NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKK 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMAEIGEDLDKSDVSSLI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 -GPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQE- 434
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                                                                                                                                                                                                                        07334/021002
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,777
FILING DATE: 31-DEC-1997
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,200
FILING DATE: 27-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08852782
Patent No. 6008042
GENERAL INFORMATION:
                                                                                                                                                                    NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REGISTRATION NUMBER: 0733
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                         TELEFAX: 61//
TELEFAX: 61//
TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
""PR: amino acid
""PR: amino acid
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FRAGMENT TYPE: internal
US-09-001-777-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FSKERSSSLEGSPDEFSNGEELCGVMTISDSPRE-----
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithfiline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                        OCHITICATION COMPORTING
OPERATING SYSTEM: DOS
SOFTWARE: FESSISCO Version 1.5
CURRENT APPLICATION DATA: 05/08/852,782
RILING DATE: 05/08/852,782
CLASSIFICATION DATA: 05/08/852,782
RILING DATE: 05/010,365
FILING DATE: 05/017,454
FILING DATE: 105/017,454
FILING DATE: 17/04X 1996
APPLICATION NUMBER: 60/017,914
FILING DATE: 16/04X 1996
APPLICATION NUMBER: 60/017,914
FILING DATE: 16/04X 1996
APPLICATION NUMBER: 19/04
FILING DATE: 16/04X 1996
APPLICATION NUMBER: 00/017,914
FILING DATE: 16/04X 1996
APPLICATION NUMBER: 00/017,914
FILING DATE: 16/04X 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,344
REFERENCE/DCCKET NUMBER: P50484-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                COMPUTER 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Han, William T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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ORIGINAL SOURCE:
                                                                                                                                                                                                              COUNTRY:
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Search completed: August 13, 2003, 16:45:03 Job time : 29.7589 secs

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			21.5	• •		S. S
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 13, 2003, 16:36:59; Search time 34.9215 Seconds (without alignments) 1321.848 Million cell updates/sec Run on:

Title: Perfect score:

US-09-380-546A-2 2473 1 MSAEVIHQVEEALDTDEKEM.......EKYYVWLQHTLRKKLILSYT 480 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR_76:* 1: pir1:* ): pir2:* : pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ŋ	Description	hypothetical prote	cysteine proteinas		cysteine proteinas	cysteine proteinas		apoptosis regulato				-	caspase-9 long cha	ICE-LAP6 - human	probable membrane	structural mainten	interleukin-1 beta	interleukin-1beta	interleukin-1 beta	probable thyroid r	hypothetical serin	IL-1 beta converta	interleukin-1 beta	hypothetical prote		Ч	kinesin-related pr	inositol 1,4,5-tri	transcription anti	inositol 1,4,5-tri
SUMMARIES																														
SUM	ជ	T30761	I67437	JC5410	A55315	S64710	JC6507	A54821	B54821	<b>S</b> 55668	T30762	167436	JC7123	G02635	867803	T47626	B57511	A56084	A42677	T03719	T39052	A46495	A49429	T31008	T20038	B56084	<b>S34830</b>	A49873	E84131	A46719
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	Length	241	212	277	277	277	452	435	312	171	371	182	454	416	790	1265	418	383	404	191	1125	402	503	422	495	311	793	2671	700	2670
æ	Query	9.4	7.5	7.3	7.3	7.3	7.2	7.1	6.9	6.9	6.3	0.9	5.9	5.7	5.6	5.5	5.4	5.3	5.1	5.1	5.1	5.1	5.1	5.0	4.9	4.9	4.9		4.9	4.9
	Score	231.5	184.5	181.5	181	179.5	177.5	175.5	171	170.5	157	148	145	142	137.5	136	133.5	131	126.5	126.5	126	125.5	125	124.5	122	121.5	121.5	121	120.5	120
	Result No.	-	7	m	4	ស	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C; Accession: 167437
R; Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Endocrinology 136, 5042-5053, 1995
A; Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammallan nulosa cells of the ovarian follicle.
A; Reference number: IS3300; MUID:96042508; PMID:7588240

cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)

hypothetical prote	hypothetical prote	ranscription regu myosin-3 heavy cha	interleukin-1 beta myosin heavy chain	transcription regu	. alpha-latroinsecto	kinesin-related pr	chromosome-associa	probable nuclear p	ATP-dependent Lon	probable DEAH ATP-	hypothetical prote	CT147 hypothetical
T05113	T29145	T38774	A57511 A37352	AI1289	530355	T14156	T45706	T41023	E97224	A75135	F75216	F86509
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8.4	4.4	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6
119.5	118	116.5	115.5	115.5	115.5	115.5	115	115	114.5	114.5	114	114
30	35	3.4	36	37	38	36	40	41	42	43	44	45

## ALIGNMENTS

host

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C; Species: Homo sapiens (man)
C; Accession: A55315; S5899; J3005
R; Fernandes-Alnemni, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A; Title: CFP32, a novel human apoptotic protein with homology to Caenorhabditis elega A; Reference number: A55315; MUID:95074098; PMID:7983002
A; Accession: A55315
A; Reference number: A55315
A; Residues: 1-277 < FER>
A; Richolson, D.W.; Alli, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, Y.M., V.L.; Miller, D.K.
A; Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammal A; Reference number: S88899; MUID:95319529; PMID:7596430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Molecule type: protein
A. Residues: 29-46;176-189, E',191-193 <NIC>
A. Residues: 29-46;176-189, E',191-193 <NIC>
B. Tewari, M.; Quan, LT.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poiri
Cell 81, 801-809, 1995
A. Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable proteas
A. Recession: 139005
A. Status: preliminary
A. Molecule type: mRMA
A. Molecule type: mRMA
A. Residues: 1-189, E', 191-277 <RES>
A. Cross-references: EMBL: U26943; NID: 9857568; PIDN: AAA74929.1; PID: 9857569
C; Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 EPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIID-------CIGNETEL--L 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 HSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQ--LENSSLLEVDGPAMKNVEF 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 KAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDLHI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.3%; Score 181; DB 2; Length 277
Best Local Similarity 26.8%; Pred. No. 0.00012;
Matches 69; Conservative 40; Mismatches 102; Indels
   N; Alternate names: cysteine proteinase CPP32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 TRVNRKVATEFESFSFD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C:Date: 10-Jun-1997 #sequence_revision 170-774, 1997
Biochem. Blophys. Res. Commun. 231, 770-774, 1997
A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation A:Reference number: JC5410; MUID:97244429; PMID:9070890
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-277 < AuUx>
A:Mux
A:Residues: 1-277 < AuUx>
A:Residues: 1-277 < Auux>
A:Residues: 1-277 < Auux>
C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQLEN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 CVILSHGDEGVIFG---TNGPVDLKKLTSFFRGDYCRSLTGKPKLFIIQ---ACRG-TEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGIETDSGT--DEEMACQK----IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCS 221
                                                                                                                                                                                                                                                                                                                                                                                                                          287 HGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEIMELMDSVS-KEDHSKRSSFVCVILSHGDEGVIFG---TNGPVDLKKLISFFRGDYCR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 EERYKMKSKPLGICLIID------CIGNETEL----LRDTFTSLGYEVQKFLHLSM 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 YLAGKPKMFFIQNYVVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-212 *RES>
A;Cross-treferences: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
C;Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DCIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 HNGRSKEQRLKEQLGAQOEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLII-----
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7.3%; Score 181.5; DB 2; Length 277;
Best Local Similarity 27.6%; Pred. No. 0.00011;
Matches 67; Conservative 37; Mismatches 104; Indels 35
                                                                                                                                                                             Length 212;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                    ; Pred. No. 4.8e-05; 36; Mismatches 81:
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                7.5%; Score 184.5; 29.1%; Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPGYYSWRNSRGGSWFIQSLCAMLK 195
                                                                                                                                                                       Query Match (.35 Best Local Similarity 29.18 Matches 60; Conservative
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MLK 224
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Length 277;

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Oysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S64710; S72395
EMBO 7. 15, 1012-1020, 1996
A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 dur A;Reference number: S64710; MUD:96183185; PMID:8605870
A;Reterence number: S64710; MUD:96183185; PMID:8605870
A;Accession: S64710
A;Molecule type: mRNA
A;Residues: 1-277 <WAN>.
A;Cross-references: EMBI:U27463
R;Wang, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 V---APDQLDLLEKCLKNI---HRID-LKTKIQKYKQSVQGAGTSYRNVLQAAIQKSLKD 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 PHKQSRLSTD-TMEHSLDNGDGPPCLQVKPCTPE----FYQAHYQLAYRLQSQPRGLALV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NYVVSEGQLENSS----LLEVDGPAMK------NVEFKAQKR 390
                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-79,'A',81-146,'Y',148-277 <WAW>
A;Cross-references: EMBL:U27463; NID:g1244443; PIDN:AAB01511.1; PID:g1244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5507
C;Saccession: Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 LKKNRVVLAKQLLLSELLEHLLEKDITL--EMRELIQ----AKGGSFSQ---NVELLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLI
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A;Residues: 1-452 <SAT>
A;Cross-references: GB:U77933; NID:g2769705; PIDN:AAB96379.1; PID:g2769706
                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Indels 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 452;
                                                                                                                                            Length
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                390 RGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 7.2%; Score 177.5; DB 2;
1 Similarity 22.4%; Pred. No. 0.00039;
97; Conservative 65; Mismatches 166;
                                                                                                                                        ; Score 179.5; DB 2;
; Pred. No. 0.00015;
36; Mismatches 93;
submitted to the EMBL Data Library, May 1995
A;Reference number: S72395
A;Accession: S72395
                                                                                                                                          Query Match 7.3%;
Best Local Similarity 27.4%;
Matches 61; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caspase-2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
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apoptosis regulator ICH-1, suppressive form S - human C; Species: Homo saplens (man) C; Decies: Homo saplens (man) C; Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999 C; Accession: B54821 R; Mura, M; Bergeron, L.; Zhu, H.; Yuan, J. R; Wang, L.; Miura, M; Bergeron, L.; Zhu, H.; Yuan, J. A; 719-750, 1994 A; Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulat A; Reference number: A54821; MUID:94373811; PMID:8087842
                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
C; Species: 128-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C; Accession: A54621
R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A; Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulat
A; Reference number: A54821; MUID:94373811; PMID:8087842
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391 GLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDLHIELNGYM 450
                                               - SWYIEALTOVESER----ACDMHVA--DML 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 LRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 V---APDQLDLLEKCL---KNIHRID-LKTKIQKYKQSVQGAGTSYRNVL-----QAAI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 QKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 LGICLIIDCI--GNETEL-----LRDTFTSLGYEVQKFLHLSMHGISQILGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 ACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFF
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A; Realdudes: 1-435 CMAN.
A; Cross-references: GB:Ul3021; NID:9537291; PID:9537292
C; Keywords: alternative splicing; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.1%; Score 175.5; DB 2; Best Local Similarity 22.0%; Pred. No. 0.00049; Matches 91; Conservative. 70; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                   apoptosis regulator ICH-1, stimulatory form L - human
                                                                                                                                                                408 VKVNALIKEREGY 420
                                                                                                                       451 YDWNSRVSAKEKY 463
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-312 <WAN>
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A; Status: preliminary
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40; Conservative
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Matches 40; Conserv
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C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Accession: S55668
R;Telford, E.A.R; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;References: GB:U20824; NID:9695172; PIDN:AAC13862.1; PID:9695247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1
C;Superfamily: equine herpesvirus 2 hypothetical protein E8
                                                                                              11;
                                                                                                                           84'LRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNL 143
                                                                                                                                                                                                                                                                                                                                                 LGICLIIDCI--GNETEL-----LRDTFTSLGYEVQKFLHLSMHGISQILGQF 296
                                                                                                                                                                                                                                       60 LPKRGPQAFDAFCEALRETKQGHLEDMLLTTLSGLQHVLPPLSCDYDLSLPFPVCESCPL 119
                                                                                                                                                                                                                                                                                                           120 YKKL------RLSTDTVEHSLDNKDGPVCLQVKPCTPEFYQTHFQLAYRLQSRP 167
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N;Alternate names: MC160L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
                                                                                                                                                   |: :| ::|:| | : |: :| |: || LKKNRVVLAKQLLLSELLEHLLEKDIITL--EMRELIQ----AKVGSFSQ---NVELLNL
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                                                                                                                                                                                                                                                                             OKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKP
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                                                                                              Gaps
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                                                        Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                       ; Score 171; DB 2; Length 312; Pred. No. 0.00062; 49; Mismatches 127; Indels
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A;Cross-references: GB:U10322
C;Keywords: alternative splicing; apoptosis
                                                        6.9%;
                                                                                         76; Conservative
                                                       Query Match
Best Local Similarity
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IQ 287
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C;Accession: T30762
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B. Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host A;Reference number: 220876; MUID: 96325459; PMID: 8670425
A;Accession: T30762
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <SEN>
A;Cross-references: EMBL:U60315; PIDN:AAC55288.1
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C;Species: Mus musculus (house mouse)
C;Species: J3.Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Date: J3.Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JG7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragmen C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C; Accession: 167436
R; Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Endocrinology 136, 5042-5053, 1995
A; Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian A; Reference number: 153300; MUID:96042508; PMID:7588240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 GMTRECAGR--LLGHGFLSOYRLOVAAINNMVGSEDLRVMC-----LCAGKLLPPSCTP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 PLGICLIIDCI-----GNETE--LLRDTFTSLGYEVQKFLHLSMHGISQILGQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 FACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPRMF 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 KMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKI----SKE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: 167436
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Rosidues: 1-182 (RES>
A; Residues: 1-182 (RES>
A; Cross-references: EMBL:U34684; NID:91004368; PIDN:AAC52260.1; PID:91004369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 6.3%; Score 157; DB 2; Local Similarity 29.9%; Pred. No. 0.0064; hes 52; Conservative 25; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 148; DB 2;
32.5%; Pred. No. 0.0093;
tive 16; Mismatches 51
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A; Reference number: JC7123; MUID:20001956; PMID:10529400 A; Accession: JC7123 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-454 <fuj> A; Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942 A; Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942 A; Cross-Inflarity 24.98; Fred. No. 0.051; Best Local Similarity 24.98; Fred. No. 0.051; Matches 87; Conservative 44; Mismatches 118; Indels 100; Gang 17.</fuj>	Db 255GCPVSVEKIVNIENGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNP 312 Qy 374 EVDG-PAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 432
80 ETHLLR-NPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDL 1 :	RESULT 14 S67803 orchalls monbrane protests vnr 2300 c most (Coopbrane)
	Frontier memorate processing the process of the pro
Qy 195 KDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKS 227	R;Alt-Moerbe, J.; Schneider, C.; Moro, M. submitted to the Protein Sequence Database, July 1996 A;Reference number: S67798 A;Accesion: S67803
OY 228 IQESEAFLPQSIPEERYKMKSKPLGICLIIDCIGN 262 :	A;Molecule type: DNA A;Residues: 1-790 <ald; A;Cross-references: EMBL;274287; NID:g1431405; PID:e253369; PID:g1431406; GSPDB:GN000 A;Experimental source: strain S288C</ald; 
Qy 263 ETELLRDIFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRG 316	C;Genetics: A;Gene: SGD:ADY3; MIPS:YDL239c A;Cross-references: SGD:S0002398 A:Map position: 41.
	C; Reywords: transmembrane protein F;706-722/Domain: transmembrane #status predicted <tmm></tmm>
Db 277 CQASHLQFPGAVYGTDGCSVSIEKIVNIFNGSGCPSLGGKFKLFFIQ 323	Ouery Match 5.6%; Score 137.5; DB 2; Length 790; Best Local Similarity 19.7%; Pred. No. 0.34; Matches 102; Conservative 78; Mismatches 162; Indels 175; Gaps 23;
G02635 ICE-LAP6 - human C; Speties: Homo sapiens (man)	QY 48 GKLSVGDLAELLYRVRREDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIG 101
C, Date, 1. Dec 1399 sequence_revision No-Jun-1997 Flext_change US-NOV-1999 C;Accession: G02635 R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit, submitted to the EMBL Data Library, April 1996 A:Reference number: H01513	QY 102 EDLDKSDVSSLIFLMKDYMGRGKISKEKSFL 132  ::::::::    :
A;Accession: G02635 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA a:Post dince: 1.416 - Anna.	QY 133DLVVELEKLNIVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAG 179
A; residues: 1-410 SDBA A;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027	QY 180 TSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLG 218
Query Match 5.7%; Score 142; DB 2; Length 416; Best Local Similarity 21.1%; Pred. No. 0.072. Matches 76; Conservative 59; Mismatches 158; Indels 68; Gans 11.	Db 307 SKRLNIVQDRFRKEITIFEKIITDFONKNEKKEKNETSAKTKCKAFSQRNILVSELY 366
SSERSFLDLVVELEKLNLVAPDQLDLEKCLKNHRIDLKTKQKYKQS 1	367
IQRAGSGSRRDQARQLIIDLETRGSQALPLFIS GTSYRNVLQAAIOKSLKDPSNNFRLHNGR	QY 276 YEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCYLVSRGGSQSVYGVD 325 
96 GKLSKPTLENLTPVVLRPEIRKPEVLRPETPRPVDIGSGGFGDVGALESLRGNADLA	326
228 IQESEAFLPQSIP	DD 463QNGFAKLYPDFQDIKNLENMEQYKQLKGKIELLEKNDRI 501
DD 153YILSMEPCGHCLIINNVHFCRESGLRTRTGSNIDCEKLRRRFSS 196 OV 286 MHGISOILGOFACMPEHRDYDRFVCVIJVGRGGGGGVVGVDOF 327	
197 LHFWYEVRGDLTAKKWYLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTD	442 LHIELNGYMYDW
Oy 328 HSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSBGQLENSSLL 373	

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A;Map position: 3
A;Introns: 147/3; 226/3; 312/3; 392/2; 481/2; 571/3; 620/3; 670/1; 706/1; 752/3; 784/3;
A;Note: T5N23.30
                                                                                                 C; Accession: T47626
R; Obermaler, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, K.; Submitted to the Protein Sequence Database, March 2000
A; Reference number: Z24463
A; Accession: T47626
rructural maintenance of chromosomes (SMC)-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AEKHLRLOEELKALKRERFLWQLYNIENDIEKANEDVDSEKSNRKDVMRELEKFEREAGK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 LSVGD---LAELLYRVRRF----DILKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 RKVEQAKYLKEIAQREKKIAEKSSKLGKIVSIPWKSVQPELLRFKEEIARIKAKIETNRK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:: |: :: |: 385 QLQDYFRLKEEAGMKTIKLRDEHEVLERQRRTDLEALRNLEENYQQLI-----NRKNDLD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAIQKSLKDPSNNFRLHNGRSKEQ--RLKEQLGAQQE------PVKKSIQESEAFL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 PQSIPEERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 FACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSG------LPLHHIRR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 --CRPNRKKYN--LAVTVAMGREMDAVVVEDENTGKDCIKYLKEQRLPPMTFIPLQSVRV 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 DLDKSDVSSLIFLMKDYMGRGKISKE-----KSFLDLVVELEKLNLVAPD---QLDLLEK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VRDLLDILRERGK 49
                        N;Alternate names: protein T5N23.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.5%; Score 136; DB 2; Length 1265;
Best Local Similarity 20.6%; Pred. No. 0.81;
Matches 98; Conservative 67; Mismatches 164; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FFIQNYVVSEGQLENSSLLEV 375
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A; Cross-references: EMBL: AL138650
A; Experimental source: cultivar Columbia; BAC clone T5N23 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPN-----
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Molecule type: DNA
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Search completed: August 13, 2003, 16:43:46 Job time : 37.4215 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 13, 2003, 16:34:29; Search time 84.2225 Seconds
(without alignments)
1470.690 Million cell updates/sec

Title:
Perfect score: 2473
Sequence:
i MSAEVIHQVEEALDTDEKEM......EKYYVWLOHTLRKKLILSYT 480
Scoring table: BLOSUM62
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: · 830525

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_23:*

1: \$P_archea:*
2: \$P_bacteria:*
3: \$P_tungi:*
4: \$P_human:*
5: \$P_mammal:*
7: \$P_mammal:*
7: \$P_mhc:*
10: \$P_plage:*
10: \$P_plage:*
11: \$P_rodent:*
12: \$P_virus:*
13: \$P_virus:*
14: \$P_unclassified:*
15: \$P_virus:*
16: \$P_archeap:*
17: \$P_archeap:*
17:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No. Score 1 2224 2 718.5 3 598 4 437.5 5 418.5	Match	Match Length DB	DB	ar	
2224 718.5 598 437.5 418.5			:		Description
718.5 598 437.5 418.5	89.9	462	4	Q96TE4	096te4 homo sapien
598 437.5 418.5	29.1	218	11	099MZ5	099mz5 rattus norv
437.5	24.2	418	13	QBUVG5	Oguve5 brachydanio
418.5	17.7	482	11	09JHX4	091hx4 rattus norv
	16.9	482	13	090W01	090wul gallus gall
402	16.3	476	13	0918J3	091813 brachydanio
386	15.6	7.8	9	Q8MJ18	O8m118 macaca mula
361	14.6	200	13	091864	Ogib64 xenopus lae
342.5	13.8	520	13	Q9IB62	091b62 xenopus lae
334	13.5	522	4	Q8IUP5	Ogiup5 homo sapien
318.5	12.9	479	4	QBWYQB	Q8wyq8 homo saplen
245	6.6	182	12	099CX0	099cx0 bovine herp
234	9.5	188	12	P88961	P88961 kaposi's sa
227	9.5	496	Ŋ	081749	081749 suberites d
220.5	8.9	283	13	093417	093417 gallus gall
197.5	0.8	400	S	OBITP2	08itp2 branchiosto

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## ALIGNMENTS

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RESULT 1

096TE4 PRELIMINARY; PRT; 462 AA.

C 096TE4;

O1-DEC-2001 (TTEMBLICAL. 19, Created)

DT 01-DEC-2001 (TTEMBLICAL. 19, Last sequence update)

DE 03003 (TTEMBLICAL. 19, Last sequence update)

C 04 MELTARID beta.

S Homo saplens (Human).

C DIART-2003 (TTEMBLICAL. 23, Last annotation update)

NOBLITARID-9606;

RA MELTARID-9606;

RA MATINGAL 21100893; PubMed-11161814;

RA MEDLINE-21100893; PubMed-11161814;

RA MATINGALD D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,

RA MATINGALD D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,

RY Cloning and characterization of three novel genes, ALS2CR2,

RY Cloning and characterization of three novel genes for ALS2.";

RY CLONING ACASTA, In the juvenile amyotrophic lateral sclerosis (ALS2)

RY CLILICAL region at chromosome 2433-434; Candidate genes for ALS2.";

RY CHILL AB038967; BAB32552.1; JOINED.

DR REMEL, AB038967; BAB32552.1; JOINED.

DR RICE-PTC; IPR001399; ICE_P20;

DR REMEL, AB038967; BAB32552.1; JOINED.

DR REMEL, AB038967; BAB32552.1; JOINED.

DR REMEL, AB038967; BAB32552.1; JOINED.

DR RICE-PTC; IPR001399; ICE_P20;

DR REMEL, AB038967; BAB32552.1; JOINED.

DR REMEL, AB038967; B
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418 AA;
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01-MAR-2002 (
01-OCT-2002 (
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                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                      RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
                                                                                                                                                                                                                                                                                                                                                                         BERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSEGQLENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                               GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT
                                                                                                                                                                                                                                                                                                  SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                            1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                         Gaps
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 Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 718.5; DB 11; Length; Pred. No. 1e-41; 24; Mismatches 28; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiao C.W., Asselin E., Tsang B.K.;
"FLIP mRNA expression in rat ovarian granulosa cells.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF244366; AAK28358.1; -.
InterPro. IPR001875; DED.
Pfam; PF01385; DED.
SMART; SM00031; DED; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
 Score 2224; DB 4;
Pred. No. 1.2e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AA.
                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.1%;
71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLYLQCLSQKLRQER 435
 89.9%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 71.6 nes 149; Conservative
Query Match 89.9
Best Local Similarity 99.8
Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLIP short form.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMK 117
GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LMFQMKRYDLLRKVFGTNKQQVE-GILRKERVISDYRVLMADVSENLDKEDLQSLIFLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILPKERSTRATSFLDVVVELEKLNEVSCEKLDFLEKCLKNIRRNDLVKKIQAYRNGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VIHOVEEALDTDEKEMLLFLCRDVAIDVVPPNVR-DLLDILRER----GKLSVGD--LAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LPQSIPE-----ERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed-10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98021435; PubMed-9380701;
Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
"CLARP, a death effector domain-containing protein interacts with caspase-8 and requiates apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.2%; Score 598; DB 13; Length 4 Best Local Similarity 33.8%; Pred. No. 4.4e-33; Matches 156; Conservative 88; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inchara N., Nunez G.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; FA448261; AAL41007.1;
InterPro; IPR001875; DED.
InterPro; IPR001309; ICE.
InterPro; IPR001309; ICE.
SMART; SM00115; CASC; 1.
SWART; SM00031; DED; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47619 MW; C2ECB3AE571E0237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                 | | | | | | | | SNWNALQASLPKLSIKE----HLYNSR 207
                                                                                                                                                                                                                                                                                                                     418
                                                                                                                 SYRNVLQAAIQK-SLKDPSNNFRLHNGR
                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zebrafish.";
Cell Death Differ. 7:509-510(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50208; CASPASE_P20; 1. PROSITE; PS50168; DED; 2.
                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, TrEMBLrel. 20, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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262

267 322

224

432

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119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 LEEDSSSYKNY-----IPDEADFLLGMATVKNCVSYRDPTRGTWYIQSLCQSLR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | | | | :| : | : | : | : | | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 1
                                                                                                                                                                                                                             ----STERRMSTE-GGEELPVSVLDEVTIKMQDMW
                                                                                                                                                                                                                                                                                                                                                          212 DSPGEQESESLNSDNV----YQMKSKPRGYCLIFNNNNFSKAREDIPKLSNMRDRKGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 GVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQ-----NY-----VVSEGQLENSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 LEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AEVIHOVEEALDTDEKEMLLFLCRD-VAI---'-DVVPPNVRDLLDILRERGKLSVGD---
                                                                   263 ETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galius gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                 GTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPV-----
                                                                                                                                                                                                                                                                                                 -KKSIQESEAFLPQSIPEERYKMKSKPLGICLI-----IDCIGN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 QE--RKRPLLDLHIELNGYMYDWNSRVSAKE--KYYVWLQHTLRKKL 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barton S., Bridgham J.T., Johnson A.L.;
"Caspase-8 and -9 expression in the hen ovary.";
Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057939; AAL23700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54645 MW; 8E3936B6EE090BEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              090WU1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE; PSO1121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50168; DED; 2.
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InterPro; ITR001875; DED.
InterPro; ITR001338; ICE.
InterPro; ITR001339; ICE.P10.
InterPro; ITR001309; ICE.P20.
Pfam; PF00455; ICE.P10; 1.
Pfam; PF00455; ICE.P20; 1.
Pfam; PF00456; ICE.P20; 1.
PRINTS; PR00376; ILIBCENZYME.
SWART; SW00115; CASC; 1.
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Matches 145; Conservative
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                                                                                                                                         SLIGLKETQKVLEDLS---LNRILQRVRC-----FVCCLISRGTNTHLLATDSNRL 326
                                                                                                                                                                                                                                                                      GLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQLENS---SLLEVDGPAMKNVEFK 386
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-----EVQKFLH-LSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Cerebellum;
Cao G., Graham S.H., Chen D., Chen J.;
"Molecular cloning and characterization of rat caspase-8: Its
implication in delayed neuronal cell death after ischemia.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AFZ19308; AAR83778.1; -.
EMBL; AFZ98372; AAK83055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dawley;
Itoh T., Itoh A., Pleasure D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     376 -QCSNTGSVPMPADVLWSVCTAEVKLLEES-GHQSVYLNALN 415
                                                                                                                                                                                                                                                                                                                                                   AQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLS 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001875; DED.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF01335; DED; 2.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
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SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                               181 NLLGEG----EMLVTEGORS------STGA---PEDSAIWLASS 211
                                                                                                                                                                                                                                                                                                                                  LAELLYRVRRFDLLKRILKMDRKAVETHL-LRNPHLVSDYRVLMAEIGEDLDKSDVSSLI 113
                                                                   FLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQ 173
SQLLFVISEALDRTELASLKFLSLEHVTVRKREDIEEP--KAFFQALQEKGMIEVGDLFF 61
                                                                                                                                                                                                                                                                                                                                                                                                LLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDLINE-20373792; PubMed-10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Tremblrel. 15, Created)
(Tremblrel. 15, Last sequence update)
(Tremblrel. 23, Last annotation update)
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cell Death Differ. 7:509-510(2000).
EMBL; AF773220; AAF79207.1; -.
HSSP; Q15806; 1QDU.
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SMART; SM00031; DED; 2.
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01-OCT-2000
01-MAR-2003
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Q918J3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 EDAGIIVLRKIPIEADFLIGMATVEHYLSYRHTKKGSIFIQELCKKMEELCPKKEDMLSI 441
                                                                                                                                                                                      1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Caspase-dependent and -independent cell death pathways characterize pathogenic Simian Immunodeficiency Virus infection. Relationship with disease evolution."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF530077; AAM95637.1; -...

EMBL; AF530077; AAM95637.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | | | | | || || || || || 327 PVEIREVTLPFAG--CRTLASKPKLFFIQ---ACQGDENQAGVWTSDGREDAPEEDEEYE
                                                                                                                                                                                                                       226 KSIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIG--NETELLRDT-----F
                                                                                                                                                                                                                                                                                                                                                                                                  110 SSLIFIAKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLD----LLEKCLKNIHRIDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 TKIQKYKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGL
                                                                                                                                       Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Flice/caspase-1 inhibitory protein (Fragment).
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus caque).
Mammalia; Butheria; Primates; Craniata; Vertebrata; Euteleostomi;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
Monceaux V., Ho Tsong Fang R., Hurtrel B., Amelsen J.-C.,
                                                                                                                                       80;
                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 78;
                                                                                                                                    Indels
                              FD9DFF4B3C3C1FB9 CRC64;
                                                                                16.3%; Score 402; DB 13; 27.4%; Pred. No. 1.5e-19; ive 97; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 HIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLIL 477
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Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
     3D; 2.
54890 MW;
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96.2%;
                                                                          Ouery Match 16.3%
Best Local Similarity 27.4%
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PROSITE; PS50168; DED; SEQUENCE 476 AA; 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388
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us-09-380-546a-2.rspt

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323 GVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEGQLENSSLLEVDGPAMKN 382
                                                                                                                                                                                                                                                                                                                                                                                                                 400 SFYEPDANG-SHLPLEADFLTAFATVEDYTSLRHRENGSIYIQQLCKALTTYTNQDLIDI 458
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                                                                                                                                                                        : | : | : | : | : | : | 290 DAEEITRIFNARGYITEEHRDLTAANIQKTLEMYS-KKDHAEKDSFVCFILSHGGVGTVC
                                                                                                                                                                                                                                                                              230 TPQPETESDYCQPQQHSHMNLETYHLEKNPHGWCVVINNYDFKEARSODCKYTDREGTAK
                                                                                                                                        263 ETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVY
                                                                                                                                                                                                                                                                                                                                                           383 VEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mphbha, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Xenopus laevis caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 QVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59626 MW; 33164A5A09CA6615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 HIELNGYMYD-----WNSRVSAKEKYYVWLQHTLRKKLIL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                  --ERYKMKSKPLGICLII-
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Nakajima K., Takahashi A., Yaoita Y.;
"Structure, expression and function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.";
J. Biol. Chem. 275:10484-10491(2000)
EMBL; AB038173; BAA94751.1; --
HSSP; Q15806; 100U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF001335; DED; 2.
Pfam; PF00655; ICE_P20; 1.
Pfam; PF00656; ICE_P20; 1.
Pfam; PF00656; ICE_P20; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00115; CASC; 1. SMART; SM00031; DED; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001875; DED
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Q9IB62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 DYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 KLLFEISEDLDKTETLAMIFICEKRVTAQEKENIKDAKTLFLCLKKKDLICYNDLSFLKE 78
                                                                                  178 AGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQE---SEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRD---LLDILRERGKLSVGDLA---E
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     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20209426; PubMed-10744739;
Nakajima K., Takahashi A., Yaoita Y.;
"Structure, expression and function of the Xenopus laevis caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
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2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01121; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS50168; DED: 2.
PROSITE; PS00255; INTERLEUKIN_7_9; 1.
SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           500 AA
  Mismatches
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InterPro: IPR001309; ICE_p20.
InterPro: IPR001309; ICE_p20.
Pfam: PF01335; DED; 2.
Pfam: PF01335; ICE_p10; 1.
Pfam: PF00655; ICE_p10; 1.
PRINTS: PR00556; ICE_p20; 1.
PRINTS: PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                               242 ERYKMKSKPLGICLIIDC 259
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                                                                                                                                                                                            61 ERYKMKSKPLGICLIIDC 78
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InterPro; IPR002398; ICE.
Conservative
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75;
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Matches
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Hadano S., Yanagisawa Y., Skapu J., Fichter K., Nasir J.,
Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
Ikeda J.-E., Hayden M.R.,
Inclair Salasa J., Hayden J.,
In Conding and characterization of three novel genes, ALS2CR1, ALS2CR2,
and ALS2CR3, in the juvenile amyotrophic lateral scierosis (ALS2)
If and ALS2CR3, in the juvenile amyotrophic lateral scierosis (ALS2)
If cenomics 71:200-213(2001).
In EMBI, AB038973; BAB32553.1; JOINED.
IN EMBI, AB038977; BAB32553.1; JOINED.
IN EMBI, AB038977; BAB32553.1; JOINED.
InterPro; IPR002198; ICE.
InterPro; IPR002198; ICE.
IN InterPro; IPR002198; ICE.
IN InterPro; IPR002198; ICE.
IN InterPro; IPR002198; ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 PTSLQD----SIPAEADFLLGLATVPGYVSFRHVEEGSWYIQSLCNHLKKLVPRHEDILS 478
                                                           DQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNYVVSEG-QLENSSLLEVDGPAMKNV 383
                                                                                                                                                                                              EFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ--ERKRPLLD 441
---YRMNRNHRGLCVIVNNHSFTSLKDRQGTHKDA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 VEEALDIDEKEMLLFLCRDVAIDVVP-----PNVRDLLDILRERGKLSVGD---LAEL
                                      ELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%; Score 318.5; DB 4; Length 26.5%; Pred. No. 8e-14; Live 79; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54565 MW; 1317FD7A4EE003FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                           442 LHIELNGYMYDWNSRVSAK--EKYYVWLQHTLRKKLI 476
                                                                                                                                                                                                                                                                                                  479
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SMART; SM00115; CASC; I.
SMART; SM00031; DED; 2.
PROSITE; PS01122; CASPASE_CYS; I.
PROSITE; PS01121; CASPASE_RIS; I.
PROSITE; PS50207; CASPASE_P10; I.
PROSITE; PS50208; CASPASE_P10; I.
PROSITE; PS50168; DED; 2.
SEQUENCE 479 AA; 54565 MW; 13176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-21100893; PubMed=11161814;
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
256 MQGASANTLNSETSTKRAAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01335; DED; 2.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-MAR-2002
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                                                                                                203
                                                                                                                                    166 LKIIEKYKERGDKLHRPEIGLMQPSAPPDYEHELINPHLSIQVSSKDNESWDEGIESLIE 225
                                                                                                                                                                                                                  226 HNGTILGEAEKEDDESGNIDHQLSDLRLNSEVTPQASLQMELYHMNHKHRGYCLIIDNSI 285
                                                                                                                                                                                                                                                       259 -CIGNETE-----LLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVC 310
                                                                                                                                                                                                                                                                               286 FMKGKRREGSDKDAGALSDVFSWLGLEVEIVKNLGTEQIRGCLKRFK-SKDHSERDCFVC 344
                                                                                                                                                                                                                                                                                                                                     311 VLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQN----YVVSEGQ 366
                                                                                                                                                                                                                                                                                                                                                                         345 CILTHGESGTVMGSDDKE--VSIREVMSYFTATSCISLTLKPKLFFIQACQGIYTHPSSK 402
                                                                                                                                                                                                                                                                                                                                                                                                              367 LENSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 LSQKLRQ--ERKRPLLDLHIELNGYMYDWNSRVSAKE-----KYYVWLQHTLRKKLI 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KYKQSVQG----AGTSYRNVLQAAIQKSLKDP---SNNFRLHNGRSKEQRLKE
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                    DKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDL
                                          165 KTKIQKYKQ-----SVQGAGTSYRNVL--QAAIQKSLKDPSN-----NFRL
                                                                                                                                                                             204 HNGR--SKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIID---
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Caspase 10, apoptosis-related cysteine protease.
Homo sapiens (Human).
Eukaryotasi Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC042844; AAH42844.1; -.
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SEQUENCE
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                                119 YMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLE-----KCLKNIHRIDLKTKIQK 170
                                                                                                                                                                                          227 ---- LPRAAV--- YRMNRNHRGLCVIVNNHSFTSLKDRQGTHKDAEILSHVFQWLGFTVH 279
                                                                                                                                                                                                                                                                                                                                                                                             391 ADFLLGLATVPGYVSFRHVEEGSWYIQSLCNHLKKLVPRHEDILSILTAVND---DVSRR 447
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                                                    280 IHNNVTKVEMEMVLQKQKCNPAHADGDCFVFCILTHGRFGAVYSSDE--ALIPIREIMSH
                                                                                              171 YKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQE
                                                                                                                               ------EEELVSQTD-VKTFLEA
                                                                                                                                                             SEAFLPQSIPEERYKMKSKPLGICLII------DCIG--NETELLRDTFTSLGYEVQ
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                                                                                                                                                                                                                                                                                              FMGDSCPYLAGKPKMFFIQNYVVSEG-QLENSSLLEVDGPAMKNVEFKAOKRGLCTVHRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome Sequence of Bovine Herpesvirus 4, a Bovine Rhadinovirus, and Identification of an Origin of DNA Replication.";
J. Virol. 75:1186-1194(2001).
EMBL: AF318573; AA807993.1; -.
InterPro; IPR001875; DED.
Pfam; FR0135; DED.
PROSITE; PS50168; DED; 2.
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MEDLINE-20583805; Pubmed-11152491;
Zimmermann W., Broll H., Ehlers B., Buhk H.-J., Rosenthal A.,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AA
                                                                                                                               197 VTPPVDKEAESYQG------
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01-JUN-2001
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Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
Neipel F., Mattmann C., Burns K., Bodmer J.L., Schroter M.,
Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.
"Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
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                                                                                                                                                                                                                                                                                                                                          MEDINE-97094384; Pubmed-8939871;
Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
"Molecular mimicry of human cytokine and cytokine response pathway
                                                                                                             Kaposį's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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S.;
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Cell-homologous genes in the Kaposi's sarcoma-associated human herpesvirus 8: determinants of its pathogenicity?";
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Nelpel F., Albrecht J., Fleckenstein B.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR011875; DED.
Pfam; PF013135; DED: 2.
SMART; SMO0313; DED; 2.
PROSITE; PS50168; DED; 2.
SRQUENCE 188 AA; 21474 MW; 37CFE147EAE45371 CRC64;
                                               Last sequence update)
Last annotation update)
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188
                                Created)
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MEDLINE-99329221; PubMed-10400794;
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                           01-MAY-1997 (TrEMBLrel. 03, 01-JUL-1997 (TrEMBLrel. 04, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                           Science 274:1739-1744(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death receptors.";
Nature 386:517-521(1997).
                                                                            FLICE inhibitory protein.
PRELIMINARY;
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413 ADFFYGFATPLGYAAYRSRRHGSWYISELCQVF---IKHPFTH---SLGSMMKKVNNRVS 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 KNPHGICLIINNHQFYHSDPEKCHSNRGGAHIDVHNLTQTFKYLRYKVEVVENISSSEMN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 QILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGL-PLHHIRRMFMGDSCPYLA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 KVMLRKA-SEDHPQYDSFVCIIMTQGGSNIVHGADSEAVNLYDLTGVMKM----CPTLR 363
                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 GKPKMFFIQNYVVSEGQLENSSLLEVDGPAMKNVEFKAQKRGL-------CTVHRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKPKIFFVQ---ACRGDIESM-----GFKNEEVSKTEDDLQADMPGGHLHTDTIPQE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVS 458
                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 DLLDILRERGKLSVGDLAE-LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 HRLGQSTSKIANKEDQIAKLQKEIKKQQERIETQVRGHVDQMQHILNTIQGLETL----
                                                            4 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY
                                                                               20 NLMDIPENVQTDSCAELEDPFLQSAQPFGLTFDPFKNDSDGEYTSIPKNDTSLTQQEQLL
                                       Gaps
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8
                                                                                                                                                                                --GSRSTPQTFLHWVYCMENLDLIGPTDVDALMSMLRSLSRVDLQRQVQ 168
                                                                                                                                                                 121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQ 169
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Wiens M., Batel R., Ammar M.S.A., Schroeder H.C., Mueller W.E.,
"Okadat catel a defense molecule in sponges.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ426651; CAD20233.1;
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SEQUENCE 496 AA; 56695 MW; 8478AB4BE68649D4 CRC64;
                                                                                                                                                                                                                                                                                                                                               Suberites domuncula (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha; Hadromerida; Suberitidae; Suberites.
NCBI_TaxID=55567;
            Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.2%; Score 227; DB 5; Length 49
23.0%; Pred. No. 1.6e-07;
tive 81; Mismatches 199; Indels
                                     Indels
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                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Caspase_related protein.
                                       64;
          ; Score 234; DB 12;
; Pred. No. 1.5e-08;
39; Mismatches 64;
                                                                                                                                                                                                                                                          496 AA.
                                                                                                                                                                                                                                                           PRT;
         9.58;
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Matches 112; Conservative
                                   58; Conservative
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        Query Match
Best Local Similarity
                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 FKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSGKLRQE-RKRPLLDLH 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 -----FTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 ASVREVFMKLGYKVKLNNDLSSRDIFKLLKNVS-EEDHSKRSSFVCVLLSHGDEGLFYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Caspase-3.
Caniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20149872. PubMed-10684799;
Johnson A.L., Bridgham J.T.;
"Caspase-3 and -6 expression and enzyme activity in hen granulosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 PVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161242DDEFD4DC4F CRC64;
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283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%; Prea, ... +1ve 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: August 13, 2003, 16:42:30 ne : 86.2225 secs
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PS502081E; PS50208; CASPASE_P20; SEQUENCE 283 AA; 31675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Reprod. 62:589-598(2000)
EMBL; AF083029; AAC32602.1; -.
HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_pl0.
InterPro; IPR001399; ICE_pl0.
Pfam; PF00655; ICE_pl0; I.
Pfam; PF00656; ICE_pl0; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
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244 TRVNRRVAEYES 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                         Gallus.
NCBI_TaxID=9031;
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